



Sequence Listing

Ashkenazi, Avi
Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Ian
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul C.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillar, Kenneth J.
Kjavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Pagni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tamas, Daniel
Williams, P. Mickey
Wood, William I.

0120 Secreted and Transmembrane Polypeptides and Nucleic
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245	250	255
Pro Ile Val Asn	Leu Phe Val Ser Arg	Asp Leu Gly Gly Ser Ser
260	265	270
Ala Ala Thr Glu	Ala Val Ala Ile Leu	Thr Ala Thr Tyr Pro Val
275	280	285
Gly His Met Pro	Tyr Gly Trp Leu Thr	Glu Ile Arg Ala Val Tyr
290	295	300
Pro Ala Phe Asp	Lys Asn Asn Pro Ser	Asn Lys Leu Val Ser Thr
305	310	315
Ser Asn Thr Val	Thr Ala Ala His Ile	Lys Lys Phe Thr Phe Val
320	325	330
Cys Met Ala Leu	Ser Leu Thr Leu Cys	Phe Val Met Phe Trp Thr
335	340	345
Pro Asn Val Ser	Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val Asp
350	355	360
Phe Ala Phe Ala	Glu Leu Cys Val Val	Pro Leu Arg Ile Phe Ser
365	370	375
Phe Phe Pro Val	Pro Val Thr Val Arg	Ala His Leu Thr Gly Trp
380	385	390
Leu Met Thr Leu	Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser Val
395	400	405
Leu Arg Ile Ile	Val Leu Ile Ala Ser	Leu Val Val Leu Pro Tyr
410	415	420
Leu Gly Val His	Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu Ala
425	430	435
Gly Phe Val Gly	Glu Ser Thr Met Val	Ala Ile Ala Ala Cys Tyr
440	445	450
Val Tyr Arg Lys	Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala Thr
455	460	465
Glu Gly Glu Asp	Ser Ala Met Thr Asp	Met Pro Pro Thr Glu Glu
470	475	480
Val Thr Asp Ile	Val Glu Met Arg Glu	Glu Asn Glu
485	490	

<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
tjagctttctg gtgccttttg gctctaattc tggccacaca gagaancagt 100
eggccatttg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
agccacagag gcajtggcga ttttgacagc cacataacct gtgggtcaca 200
tgcatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
ggccacatc aagaagttca ccttcgtctg catggtcttg tcactcacgc 350
ctgtttctgt gatgttttg acacccaacg tgtctngaa aatcttgata 400
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450
ggggatcttc tctttcttcc cagttccagt cacagtgagg ggcctctca 500
cgggtgggt gatgacactg aagaaaacct tggtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tgacggaatc ccgggtggg tatcctggtt tngacaagat aaacccccag 50
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100
agttcaacct ngtttgnatg gntctgtcaa ctacgctnt gtttcgtgat 150
gttttgagca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200
tggantttgc ctttgacagaa ntttgnntg ttcttttgcg gattttctcc 250
tttttccag ttccagtcac agngaggjcg catctcaccg ggnngntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350
ttgtcctnat ngccagcctt gtggctctac cctacctggg ggtgcacggt 400
gggaccttg gcgtaggttc cctctggcg ggca 434

<210> 10
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 49, 68, 83, 90, 98, 119
<223> unknown base

<400> 10
tattccagc tccggtcacg gggagggcgc atntcacgg gtggctgag 50
aacctgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100
cgtctctcgc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150
agac 154

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
atgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gtctgtcac tcacgtc 18

<210> 13
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcctctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttcgcgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcgaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gactgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcgggggagca ggccctgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
gccccgcgcc cggcgccggg cggccgaagc cgggagccac cggcatgggg 50
gactgactgg gagcctgctc cctgctcagc tgcgcgtcct gactctgcgg 100
ctctgccccc tgcatactgt gcagctgctg ccccgccagc cgcaactcca 150

ccgtgagcgc cctcatcttc acgttcttcc tcttcctggg ggtgctgggtg 200
tccatcatta tgetgagccc gggcgtggag agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtctgt cagggccaca 300
tcgaactgtg etccctgctt ggctaccgcg ctgtctacgc catgtgcttc 350
gccacggcgg ccttcttctt cttctttttt accctgctca tgetctgcgt 400
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450
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gacggctctt tcaccaacat ctgggtctac ttgggcgtcg tgggtcctt 550
cctcttcttc ctcatccagc tgggtgtgtc catcgacttt ggcactctt 600
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ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggtgccacg 750
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gcaggtggca gctgtgagg gcggggcctt tgacaacgag caggacggcg 1200
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caccaatcag ccaggtgag ccccccacc tgcccagct ccaggacctg 1550
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caggctcctg cagagcccac tccccccgce acaccacacac ggtggagctg 1650
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 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtaacgtc cccagggga cctgcccc ttctggact tegtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900
 a 1901

<210> 19
 <211> 457
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser
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 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
 20 25 30
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
 35 40 45
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
 50 55 60
 Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly
 65 70 75
 Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser
 80 85 90
 Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala
 95 100 105
 Ala Phe Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser
 110 115 120
 Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe
 125 130 135
 Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr
 140 145 150
 Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val
 155 160 165
 Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile
 170 175 180

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu	185	190	195
Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr	200	205	210
Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe	215	220	225
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe	230	235	240
Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala	245	250	255
Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu	260	265	270
Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser	275	280	285
Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro	290	295	300
Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr	305	310	315
Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile	320	325	330
Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His	335	340	345
Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met	350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu	365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr	380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met	395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met	410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp	425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu	440	445	450
Leu Arg Asn Arg Asp Phe Ser	455		

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
gcgcgcctcat cttcacgttc ttcc 24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
tcacccagct ggtgctgctc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 22
cttcttcac ttctgcctgg 20

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
ccttggcaca aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggatgta gaaggcacc acgg 24

<210> 25
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcaccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgtgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcagagcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctctacagt tacgtctctc 100
cgccgcacgt ccgcgaggac ttgaagtcc tgcgcctcaa gtttgtccgt 150
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
ctgttagagc atttgtccta tttcccccag tctttgtctc cgaagctgtg 250
actgccgatt cgggaagtcc tgaggagcgt cagaagcggc ttccctacgt 300
cccagagccc tattaccggg aatctggatg ggaccgcctc cgggagctgt 350
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aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agctttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
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 gtactctcac ttacttate cttaaattta aatacatact tatgtttgta 1250
 ttaattctac aatatatgca tacatggata tatccacca cctagatttt 1300
 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350
 t 1351

<210> 28
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 28
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 Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
 20 25 30
 Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val
 35 40 45
 Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu
 50 55 60
 Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala
 65 70 75
 Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val
 80 85 90
 Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile
 95 100 105
 Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val
 110 115 120
 Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly
 125 130 135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn
				140					145					150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu
				155					160					165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg
				170					175					180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly
				185					190					195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln
				200					205					210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg
				215					220					225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu
				230					235					240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg
				245					250					255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu
				260					265					270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp
				275					280					285

<210> 29
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 29
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 ctattaccgc gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggettca 300
 ttctttcatg gctggcgccg aacc 324

<210> 30
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure

<222> 262, 330, 371

<223> unknown base

<400> 30

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accgcgggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100

gtgtgcgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150

ggggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200

gontccggga gtgttttggc aaagatgaac agcagagaat ttcaaaggac 250

cttgtgtgata tntgtaagac ggcagctaca gcaggcatca ttggtctgggt 300

gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350

agagccaggc agaaatttat nataacc 377

<210> 31

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 31

tccgtacaggtt acgctctccc 20

<210> 32

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 32

cttgaggagc gtcagaagcg 20

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 33

ataacgaatg aagcctcgtg 20

<210> 34

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaataatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

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gacaaagcag ctgtcaggga acctccgcgc gagtcgaatt tacgtgcagc 150
tgcgggcaac cacagggtcc aagatggttt gcgggggctt cgcgtgttcc 200
aagaactgcc tgtgcgcctt caacctgctt tacaccttgg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg ctccgggctg atttccagtc 300
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 caattttttt tgggtctttt aggaaagatt gttgtggtaa aaagtgttag 1300
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
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 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
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 aaaagatatt tgattatctt aaaaattggt aaataccgtt ttcatgaaat 1650
 ttctcagtat tgtaacagca acttgctaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800
 taaaagaaaag taatggaag 1819

<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

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Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile
				20					25					30
Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val
				35					40					45
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
				50					55					60
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
				65					70					75
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe
				80					85					90
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly
				95					100					105

Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn
				110					115					120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn
				125					130					135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser
				140					145					150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val
				155					160					165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu
				170					175					180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp
				185					190					195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu						
				200										

<210> 37

<211> 390

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336

<223> unknown base

<400> 37

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tagccttgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150
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gttcogaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
gtgaccactn gtgctcgcaa tgtgctccaa tcataggaga atatgctgga 300
taggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350
gactctgggt gtttggctga cctacagata caggaaccag 390

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<210> 38

<211> 566

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 27

<223> unknown base

<400> 38

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tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tataatgtat aataacattt acctcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tataaaagac tgcattttta aacaagttag tattaatgag 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
cgttttcat gaaagttctc agtattgtta cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttgttttagc cctgaaaac aggagcaaca gggncagct tctggaggt 100
tggttgcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150
aatctaaaac tgetgtgggt tccgaagtgt taacccaaat gacacctgtc 200
tggctngctg tggtaaaagt gacctcgt gctcgccatg tgetccaatc 250
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40
accacgtct gcgttgetgc c 21

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
gagaatatgc tggagagg 18

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
aggaatgcac taggattcgc gcgg 24

<210> 43
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
ggccccaaag gcaaggacaa agcagctgtc aggggaacctc cgccg 45

<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 44
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 ttgtagccta a 2061

<210> 45

<211> 359

<212> PRT

<213> Homo sapiens

<400> 45

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Glu	Thr	Leu	Gln	Cys	Glu	Gly	Pro	Val	Cys	Thr	Glu	Glu	Ser	Ser	35	40	45	
Cys	His	Thr	Glu	Asp	Asp	Leu	Thr	Asp	Ala	Arg	Glu	Ala	Gly	Phe	50	55	60	
Gln	Val	Lys	Ala	Tyr	Thr	Phe	Ser	Glu	Pro	Phe	His	Leu	Ile	Val	65	70	75	
Ser	Tyr	Asp	Trp	Leu	Ile	Leu	Gln	Gly	Pro	Ala	Lys	Pro	Val	Phe	80	85	90	
Glu	Gly	Asp	Leu	Leu	Val	Leu	Arg	Cys	Gln	Ala	Trp	Gln	Asp	Trp	95	100	105	
Pro	Leu	Thr	Gln	Val	Thr	Phe	Tyr	Arg	Asp	Gly	Ser	Ala	Leu	Gly	110	115	120	
Pro	Pro	Gly	Pro	Asn	Arg	Glu	Phe	Ser	Ile	Thr	Val	Val	Gln	Lys	125	130	135	
Ala	Asp	Ser	Gly	His	Tyr	His	Cys	Ser	Gly	Ile	Phe	Gln	Ser	Pro	140	145	150	
Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165	
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180	
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195	

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

tttcacgcgc caattctc 18

<210> 48

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggaac tgtctgcact gaggagagca gtgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

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<210> 52

<211> 301

<212> PRT

<213> Homo sapiens

<400> 52

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			20					25					30
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Leu	Gln	Gly	Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Gln
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Gly	Ser	Asp	Pro	Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly
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His	Ile	Gln	Gln	Ala	Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser
			80					85					90
Lys	Val	Pro	Gly	Asp	Val	Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu
			95					100					105
Asp	Asp	Arg	Ser	His	Tyr	Thr	Cys	Glu	Val	Thr	Trp	Gln	Thr
			110					115					120
Asp	Gly	Asn	Gln	Val	Val	Arg	Asp	Lys	Ile	Thr	Glu	Leu	Arg
			125					130					135
Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr	Val	Thr	Thr	Gly	Ser
			140					145					150
Tyr	Gly	Phe	Thr	Val	Pro	Gln	Gly	Met	Arg	Ile	Ser	Leu	Gln
			155					160					165
Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	Ile	Trp	Tyr	Lys
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Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	Thr	Leu	Ser
			185					190					195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	
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Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	
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Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	
				230					235					240	
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	
				245					250					255	
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	
				260					265					270	
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	
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Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	
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Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	
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<220>
 <223> Synthetic oligonucleotide probe

<400> 53
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<210> 54
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<210> 56
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agcraaatcc agcagctggc ttac 24

<210> 57
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<210> 58
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<212> DNA
<213> Homo sapiens

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<210> 59
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 59
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 35 40 45
 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln
 50 55 60
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
 65 70 75
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
 80 85 90
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp
 95 100 105
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val
 110 115 120
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
 125 130 135
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
 140 145 150
 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr
 155 160 165
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro

170	175	180
Pro Lys Ser Arg	Ile Asp Tyr Asn His	Pro Gly Arg Val Leu Leu
185	190	195
Gln Asn Leu Thr	Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala
200	205	210
Gly Asn Glu Ala	Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val
215	220	225
Gln Tyr Val Gln	Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly
230	235	240
Ile Val Ala Gly	Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu
245	250	255
Ile Arg Arg Lys	Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro
260	265	270
Asn Glu Ile Arg	Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val
275	280	285
Lys Pro Ser Ser	Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly
290	295	300
Ser Ser Ser Thr	Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln
305	310	315
Arg Thr Leu Ser	Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr
320	325	330
Gln Ala Tyr Ser	Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro
335	340	345
Lys Lys Val His	His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro
350	355	360
Ser Met Ile Pro	Ser Gln Ser Arg Ala	Phe Gln Thr Val
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

ccagtcaca gcaggcaacg aagc 24

<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggetgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

gtatgtacaa agcctcggca tggttgcagg agcagtgaca ggc 43

<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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gggtgtggag gtagatgggc tcccgcccg ggaggcggcg gtggatgcgg 250

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ccagaacaga aggcctcaga tctcattggc acataccgc atgttgaccg 500

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tgaactgacc agaattgcct tgcctacctg gcctgttcca gtctaacct 750

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accgctatt cgaaattatt ggagtcaaga gccaggaagc cagccagacc 2250
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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

Met	Gly	Thr	Ser	Pro	Ser	Ser	Ser	Thr	Ala	Leu	Ala	Ser	Cys	Ser		1	5	10	15
Arg	Ile	Ala	Arg	Arg	Ala	Thr	Ala	Thr	Met	Ile	Ala	Gly	Ser	Leu		20	25	30	
Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln		35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala		50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr		65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser		80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys		95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys		110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro		125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys		140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp		155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro		170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln		185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val		200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro		215	220	225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu		230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu		245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile		260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys		275	280	285	

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys	Glu	Lys	Lys	Asp	Thr	Val
				575					580					585
Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp	Leu	Gln	Pro	Ile	Phe
				590					595					600
Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile
				605					610					615
Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu
				620					625					630
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp
				635					640					645
Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu					
				650					655					

<210> 65
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 65
 gtagcagtgc acatgggggtg ttgg 24

<210> 66
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 66
 aacgcacatc ctcagtctct gtcc 24

<210> 67
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 67
 acgatgatcg cgggctccct tctcttgctt ggattcctta gcaccaccac 50

<210> 68
 <211> 2412
 <212> DNA
 <213> Homo sapiens

<400> 68

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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

Met	Gly	Glu	Asn	Asp	Pro	Pro	Ala	Val	Glu	Ala	Pro	Phe	Ser	Phe
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Arg	Ser	Leu	Phe	Gly	Leu	Asp	Asp	Leu	Lys	Ile	Ser	Pro	Val	Ala
				20					25					30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35				40						45

Leu	Lys	Phe	Phe	Pro	Ile	Ile	Val	Ile	Gly	Ile	Ile	Ala	Leu	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Leu	Ala	Leu	Ala	Ile	Gly	Leu	Gly	Ile	His	Phe	Asp	Cys	Ser	Gly					
				65					70					75					
Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	Ala					
				80					85					90					
Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr					
				95					100					105					
Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe					
				110					115					120					
Thr	Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly					
				125					130					135					
His	Tyr	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr					
				140					145					150					
Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe					
				155					160					165					
Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys					
				170					175					180					
Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala					
				185					190					195					
Ser	Gly	His	Val	Val	Thr	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg					
				200					205					210					
Arg	Gly	Tyr	Ser	Ser	Arg	Ile	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu					
				215					220					225					
Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe	Gln	Gly	Tyr	His					
				230					235					240					
Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	Leu	Trp	Ile	Ile	Thr	Ala					
				245					250					255					
Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	Lys	Ser	Trp	Thr	Ile					
				260					265					270					
Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	Ala	Pro	Ser	His					
				275					280					285					
Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	Pro	Lys	Arg					
				290					295					300					
Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr					
				305					310					315					
Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu					
				320					325					330					
Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala					

	335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala	350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr	365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr	380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val	395	400	405
Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe	410	415	420
Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg	425	430	435
Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp	440	445	450
Leu Lys Thr			

<210> 70
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 70
 tgacatcgcc cttatgaagc tggc 24

<210> 71
 <211> 24
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 71
 tacacgtccc tgtggttgca gata 24

<210> 72
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 72

cggttcaatgc agaaatgatc cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

cccacgcgtc cgtcctagtc cccgggccaa ctcggacagt ttgctcattt 50

attgcaacgg tcaaggtctg cttgtgccag aacggcgcgc gcgcgcgcac 100

jcaagcacac acacgggggg aaactttttt aaaaatgaaa ggctagaaga 150

gtcagcggc ggcgcgggcg ctgcgcgagg gtcgcggagc tgactcgccg 200

aggcaggaaa tccctcgggt cgcgacgcgc ggccccggct cggcgccgcg 250

gtgggatggt gcagcgctcg ccgcggggcc cgagagctgc tgcaactgaag 300

gcgggcgacg atggcagcgc gcccgctgac cgtgtccccc gcccgcgccc 350

tctgtctcgc cctggccgggt gctctgctcg cgcctcgaga ggcccgaggg 400

gtgagcttat ggaaccaagg aagagctgat gaagttgtca gtgcctctgt 450

tccgagtggg gacctctgga tcccagtga gagcttcgac tccaagaatc 500

atccagaagt gctgaatatt cgactacaac gggaaagcaa agaactgac 550

ataaatctgg aaagaaatga aggtctcatt gccagcagtt tcacggaaac 600

ccactatctg caagacggta ctgatgtctc ctcgctcga aattacacgg 650

gtcaactgta ctaccatgga catgtacggg gatattctga ttcagcagtc 700

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 agcctaactc catccccctg ggccattact gcataaaata gagtgcattt 3300
 gaaat 3305

<210> 74
 <211> 735
 <212> PRT
 <213> Homo sapiens

<400> 74
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 Leu Ala Leu Ala Gly Ala Leu Leu Ala Pro Cys Glu Ala Arg Gly
 20 25 30
 Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala
 35 40 45
 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp
 50 55 60
 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu
 65 70 75
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile
 80 85 90
 Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp
 95 100 105
 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly
 110 115 120

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys
125 130 135

Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val
140 145 150

Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro
155 160 165

Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His
170 175 180

Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser
185 190 195

Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr
200 205 210

Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln
215 220 225

Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu
230 235 240

Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg
245 250 255

Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys
260 265 270

Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp
275 280 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala
290 295 300

Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met
305 310 315

Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile
320 325 330

Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu
335 340 345

Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu
350 355 360

Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys
365 370 375

Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser
380 385 390

Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met
395 400 405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctgacaacga aaacaaaaca gttttggggg ttcaggaggg gaantccagc 100

ctaccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150

ttgagntttt tgntaaaaca tggacatgnt tcagtgtgc tcntgagaga 200

gtagcagggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250

aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300

agcaagggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350

gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450

gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

gtctcagcac gtgttctggt ctccagg 27

<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 77
catgagcatg tgcacggc 18

<210> 78
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 78
taactgcacg atgggcac 18

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
caactgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
ctccaggtg gtctccaagt ccttcc 26

<210> 81
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
tccctgttgg actctgcagc ttcc 24

<210> 82
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 82
cttcgctggg aagagtttg 19

<210> 83
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 83
gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

<400> 84
catcctgcaa catggtgaaa ccacgcctgg ctaattttgt tgtatttttg 50
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atgactctgcc cgcctcggcc tcccaaagtg ctgggattac aggcgagtgc 150
aaccacaccc gccacaaaac tttttaagaa gttaatgaaa ccataccttt 200
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<210> 85
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 85
 Met Gly Lys Gly Met Val Ala Met Leu Ile Leu Gly Leu Leu Leu
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 Leu Ala Leu Leu Leu Pro Val Gln Val Ser Ser Phe Val Pro Leu
 20 25 30
 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
 35 40 45
 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
 50 55 60
 Ala Leu Leu His Leu Tyr His
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<210> 86
 <211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
acgggcacac tggatcccaa atg 23

<210> 87
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
ggttagagatg tagaaggga agcaagacc 29

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
gtccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89
<211> 2956
<212> DNA
<213> Homo sapiens

<400> 89
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<210> 90
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 90
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 Ala Ala Leu Thr Ala Leu Leu Leu Leu Leu Gly His Gly Gly
 20 25 30
 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala
 35 40 45

Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro	50	55	60
His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile	65	70	75
Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly	80	85	90
His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys	95	100	105
Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp	110	115	120
Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly	125	130	135
Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys	140	145	150
Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu	155	160	165
Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu	170	175	180
Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser	185	190	195
Ala Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His Phe Ile	200	205	210
Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro	215	220	225
Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val	230	235	240
Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser	245	250	255
Gly Asn Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp	260	265	270
Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser	275	280	285
Leu Arg Glu Tyr Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly	290	295	300
Ala Thr Glu Thr Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala	305	310	315
Glu Pro Glu Ala Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Asn	320	325	330

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe
335 340 345

Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp
350 355 360

Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys
365 370 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys
380 385 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly
395 400 405

Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu
410 415 420

His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu
425 430

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91

atgtttcttcg cgccttggtg 20

<210> 92

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

ccaagccaac acactctaca g 21

<210> 93

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

aagtgggtgc cttgtgcaac gtgc 24

<210> 94

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 94

ggtcacaaaggg gatatatcgc cac 23

<210> 95

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 95

gcacatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96

<211> 1016

<212> DNA

<213> Homo sapiens

<400> 96

ctttttctgag gaaccacagc aatgaatggc ttgtcatcct tgcttcgaag 50
aaaccaatctt atcctcctgg tactattttct ttgcaaatt cagagtctgg 100
gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150
atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200
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gagaactggg tgatatggga gatcagggca atattggcaa gactggggccc 300
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 aaaaaaaaaa aaaaaa 1016

<210> 97
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 97
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 20 25 30
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
 80 85 90
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
 95 100 105
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
 110 115 120
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
 125 130 135
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
 140 145 150
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
 155 160 165
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
 170 175 180
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
 185 190 195
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn		
215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser		
230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly		
245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys		
260	265	270
Glu Phe Ile Lys Lys Lys Lys		
275		

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 98
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<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 99
 gatgatggag gctccatacc tcag 24

<210> 100
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 100
 gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101
 <211> 2574
 <212> DNA
 <213> Homo sapiens

<400> 101
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gggcctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150
gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200
agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250
gtccatggc tgcctcctg ctgctgccc tgctgctgtt gctaccgctg 300
ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350
cttggccttt gcggtgcgag ctctgtgctg caaaagggt cttcgagctc 400
gcgcctggc cgcggtgcc gccgaccgg aaggtccga ggggggctgc 450
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catggcccaa cttgtttatt gcag 2574

<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gly	Val	Cys	Gln	Arg	Thr	Arg	Ala	Pro	Trp	Lys	Glu	Lys	Ser
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Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly
				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320	325		330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335	340		345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350	355		360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365	370		375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380	385		390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395	400		405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410	415		420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425	430		435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440	445		450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455	460		465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470	475		480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485	490		495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp
500	505		510
Val Thr Thr Gly	Glu Pro Ile Arg Asp	Pro Gln Gly His Cys	Met
515	520		525
Ala Thr Ser Pro	Gly Glu Pro Gly Leu	Leu Val Ala Pro Val	Ser
530	535		540
Gln Gln Ser Pro	Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu	Ala
545	550		555
Gln Gly Lys Leu	Leu Lys Asp Val Phe	Arg Pro Gly Asp Val	Phe
560	565		570
Phe Asn Thr Gly	Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe	Leu
575	580		585
Arg Phe His Asp	Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly	Glu
590	595		600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp	605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His	620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His	635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu	650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu	665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn	680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu	695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr	710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile	725	730	

<210> 103
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 103
 gagagccatg gggctccacc tg 22

<210> 104
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 104
 ggagaatgtg gccacaac 18

<210> 105
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
atccacttca gcggacac 18

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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<400> 107
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
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cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100
acggcgccat acacactcgc tctcgtttgt ccatctccct cccgggggag 150
ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagcccgc 200
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<210> 109
 <211> 555
 <212> PRT
 <213> Homo sapiens

<400> 109
 Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu
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 20 25 30
 Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala
 35 40 45
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys
 50 55 60
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu
 65 70 75
 Ser Gln Gln Ser Lys Leu Glu Phe Glu Asn Leu Val Glu Glu Thr
 80 85 90
 Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Lys Phe
 95 100 105
 Asp Glu Phe Phe Arg Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu
 110 115 120
 Asn Asp Met Phe Val Arg Thr Tyr Gly Met Leu Tyr Met Gln Asn
 125 130 135
 Ser Glu Val Phe Gln Asp Leu Phe Thr Glu Leu Lys Arg Tyr Tyr
 140 145 150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp
				440					445					450
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met
				455					460					465
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly
				470					475					480
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser
				485					490					495
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe
				500					505					510
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg
				515					520					525
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser
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Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg
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<223> Synthetic oligonucleotide probe

<400> 111

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 <212> PRT
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 35 40 45
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala
 50 55 60
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln
 65 70 75
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
 80 85 90
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys
 95 100 105
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro
 110 115 120
 Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln
 125 130 135
 Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro
 140 145 150

Asn Cys Leu Pro	Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	155	160	165
Glu Val Gly Tyr	Ser Thr His Met Val	Gly Lys Trp His Leu Gly	170	175	180
Phe Asn Arg Lys	Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	185	190	195
Phe Phe Gly Ser	Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	200	205	210
Lys Cys Asp Ser	Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	215	220	225
Asp Asn Ala Ala	Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	230	235	240
Met Tyr Thr Gln	Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	245	250	255
Thr Lys Pro Ile	Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	260	265	270
Pro Leu Gln Ala	Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	275	280	285
Ile Asn Ile Asn	Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	290	295	300
Asp Glu Ala Ile	Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	305	310	315
Phe Tyr Asn Asn	Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	320	325	330
Gln Pro Thr Ala	Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	335	340	345
Gly Thr Tyr Trp	Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	350	355	360
Ser Pro Leu Leu	Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	365	370	375
His Ile Thr Asp	Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	380	385	390
Gln Ile Asp Glu	Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	395	400	405
Thr Ile Ser Glu	Gly Leu Arg Ser Pro	Arg Val Asp Ile Leu His	410	415	420
Asn Ile Asp Pro	Tyr Thr Pro Arg Gln	Lys Met Ala Pro Gly Gln	425	430	435

Gln Ala Met Gly Ser Gly Thr Leu Gln Ser Ser Gln Pro Ser Glu
440 445 450

Cys Ser Thr Gly Asn Cys Leu Gln Glu Ile Leu Ala Thr Ala Thr
455 460 465

Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly
470 475 480

Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe
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Ser Thr Ser Gln Pro Thr His Met Arg Gly Trp Thr Tyr Leu Thr
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Gly Ile Gln Glu Ser
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<210> 116

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<223> Synthetic oligonucleotide probe

<400> 116

ctctctgagt gtacatctgt gtgg 24

<210> 117

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<220>

<221> unsure

<222> 33

<223> unknown base

<400> 117

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cgg 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
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Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
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His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
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<223> Synthetic oligonucleotide probe

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<210> 122

<211> 50

<212> DNA

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<400> 122

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<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

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gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu	Glu
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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
			20						25					30

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
			35						40					45

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
			50						55					60

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	65	70	75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	80	85	90
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	95	100	105
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	110	115	120
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	125	130	135
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	140	145	150
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	155	160	165
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	170	175	180
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser	185	190	195
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	200	205	210
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	215	220	225
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	230	235	240
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	245	250	255
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	260	265	270
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	275	280	285

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgttagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca etc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gactggcagg gacgacgcc agaattg 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131

gcgacgtggg caccgccatc agctgttcgc gcgtttcttc ctccaggtgg 50
ggcagggggtt tcgggctggt ggagcatgtg ctgggacagg acagcctct 100
caatcaatcc aacagcatat tcggttgcac cttctacaca ctacagctat 150
tggttaggttg cctgcggaca cgtcgggctt ctgtcctgat gctgctgagc 200
tccctggtgt ctctcgtctg ttctgtctac ctggcctgga tctgtttctt 250
cgtgctctat gatttctgca ttgtttgtat caccacctat gctatcaacg 300
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<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

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Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
			20						25					30

Ile Thr Thr Tyr Ala	Ile Asn Val Ser Leu Met Trp Leu Ser Phe	35	40	45
Arg Lys Val Gln Glu	Pro Gln Gly Lys Ala Lys Arg His Gly Asn	50	55	60
Thr Val Pro Gly Glu	Trp Pro Trp Gln Ala Ser Val Arg Arg Gln	65	70	75
Gly Ala His Ile Cys	Ser Gly Ser Leu Val Ala Asp Thr Trp Val	80	85	90
Leu Thr Ala Ala His	Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu	95	100	105
Asn Ser Trp Ser Val	Val Leu Gly Ser Leu Gln Arg Glu Gly Leu	110	115	120
Ser Pro Gly Ala Glu	Glu Val Gly Val Ala Ala Leu Gln Leu Pro	125	130	135
Arg Ala Tyr Asn His	Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu	140	145	150
Gln Leu Ala His Pro	Thr Thr His Thr Pro Leu Cys Leu Pro Gln	155	160	165
Pro Ala His Arg Phe	Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly	170	175	180
Trp Asp Gln Asp Thr	Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu	185	190	195
Arg Leu Arg Leu Ile	Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn	200	205	210
Gln Leu His Gln Arg	His Leu Ser Asn Pro Ala Arg Pro Gly Met	215	220	225
Leu Cys Gly Gly Pro	Gln Pro Gly Val Gln Gly Pro Cys Gln Gly	230	235	240
Asp Ser Gly Gly Pro	Val Leu Cys Leu Glu Pro Asp Gly His Trp	245	250	255
Val Gln Ala Gly Ile	Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu	260	265	270
Asp Ala Pro Val Leu	Leu Thr Asn Thr Ala Ala His Ser Ser Trp	275	280	285
Leu Gln Ala Arg Val	Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro	290	295	300
Glu Thr Pro Glu Met	Ser Asp Glu Asp Ser Cys Val Ala Cys Gly	305	310	315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	320	325	330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	335	340	345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	350	355	360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	365	370	375
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly	380	385	390
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu	395	400	405
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys	410	415	420
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp	425	430	435
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln	440	445	450
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu	455	460	465
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met	470	475	480
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu	485	490	495
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu	500	505	510
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg	515	520	525
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser	530	535	540
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu	545	550	555
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser	560	565	570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcacc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggcgcgcc ccggccccca ttggggccgg gcctcgctgc ggcggcgact 50

gagccaggct gggccgcgtc cctgagtcac agagtcggcg cggcgcgcca 100

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gatgtgcgt cggcggggca gccctggcat ggggtgtgcat gtgggtgcag 200

cctggggagc actgtggttc tgccctcacag gagccctgga ggtccaggtc 250

cctgaagacc cagtgggtggc actggtgggc accgatgcca cctgtgctg 300

ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agataccaaa cagctggtgc acagctttgc tgagggccag 400

gaccagggca ggcctatgc caaccgcag gccctcttcc cggacctgct 450

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attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

Met	Leu	Arg	Arg	Arg	Gly	Ser	Pro	Gly	Met	Gly	Val	His	Val	Gly	
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				20					25					30	
Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	
				35					40					45	
Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	
				50					55					60	
Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	
				65					70					75	
Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	
				80					85					90	
Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	
				95					100					105	
Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	
				110					115					120	
Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	
				125					130					135	
Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu	
				140					145					150	
Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys	
				155					160					165	
Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	
				170					175					180	
Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	
				185					190					195	
Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val	
				200					205					210	
Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	
				215					220					225	

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln
				230					235					240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu
				245					250					255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys
				260					265					270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala
				275					280					285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln
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Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
				305					310					315

Ala

<210> 138
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 138
 ctggcacagc tcaacctcat ctgg 24

<210> 139
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 139
 gctgtctgtc tgtctcattg 20

<210> 140
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 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

<400> 140
 ggacacagta tactgaccac 20

<210> 141
 <211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 141

tgcaaccag gcagctgtaa gtgc 24

<210> 142

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 142

tggaagaaga ggggtgtgat gtgg 24

<210> 143

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 143

gagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144

<211> 2336

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1620, 1673

<223> unknown base

<400> 144

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gaagggggag tctgaactt gtctgaagcc cttgtccgta agccttgaac 100

taagttctta aatctatgaa gtcgaggac ctttcgctgc ttttgtaggg 150

aattctttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcggtc 200

ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250

agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300

aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350

ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatattg 400

gtttaccctg ggcacccctg aggcctctcaa aggttgggac cagggcctga 450
aaggaatgtg tgtaggagag aagagaaaagc tcatcattcc tectgctctg 500
ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550
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cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650
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tgaaagtcac catgatgctt tggaggagga tatttttgat aaagaagatg 750
aagacaaaaga tgggtttata tctgccagag aatttacata taaacacgat 800
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cggtaaagcg agatcacctn cagcctggac actctgtctc gaaaaagaa 1650
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tcaatatggt atagatgagg tagaaagtta tatttatatt caatatttac 1850
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 aggcgggaggt tgcagtgagc caagattgtg ccaactgcact ccagcctggg 2250
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<210> 145
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 145
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 Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu
 20 25 30
 Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
 35 40 45
 Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
 50 55 60
 Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
 65 70 75
 Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
 80 85 90
 Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
 95 100 105
 Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
 110 115 120
 Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
 125 130 135
 Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
 140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu
200 205 210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 146

ctttccttgc ttcagcaaca tgaggc 26

<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

gccagagca ggaggaatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

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tttttttagc atccaaccat tcttcccttg tagttctcgc cccctcaa 100
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cagagatgcc tggctacctc gccctgccct cagcctcacc gggctcagtc 200
tctttttctc tttggtgcca ccaggacgga gcatggaggt cacagtacct 250
gccaccctca acgtcctcaa tggctctgac gcccgccctgc cctgcacctt 300
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350
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tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150
<211> 215
<212> PRT
<213> Homo sapiens

<400> 150
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35 40 45
Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His
50 55 60
Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys
65 70 75
Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu
80 85 90
Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro
95 100 105
Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu

110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg		
125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu		
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser		
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val		
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp		
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro		
200	205	210
Asp Asp Gly Ala Lys		
215		

<210> 151
 <211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
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 tectcccttg tagttctcgc cccctcaaatt cactttctcc cttagcccac 100
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 gccctgcctt cagcctcagc gggtcagtc tctttttctc tttggtgcca 200
 ccaggacgga gcatggaggt ccacagtacc tgnccacct caacgtcctc 250
 aatggctctg acgcccgcct gccctgcct tcaactcctg ctacacagtg 300
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
 ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400
 tggagcgggt tcaagaccgc gtggagttct cagggaaacc cagcaagtac 450
 gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
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gaggtncaca tacctgccac cctcaacgtc ctcaatgget ttgacgcccg 100
cctgccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150
ccctgaactg gatttaccag gagtgcaca actggctctg aggagatgtt 200
cctccagttc ccgcatggaa gatcatttaa cctgaaaget ggaagcgggt 250
ttcaagaacc gcgtggaagt ttctcagga accccagcaa gtacgatgtg 300
tcgggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350
ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155

cgctgcct gcaccttcaa ctctgtctac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

tgcggcgacc gtctacacc atgggcctcc acctccgcc ctaccgtgtg 50

gggtctctcc cggatggcct cctgttctc ttgtctctgc taatgtctgt 100

cggggaccca gcgtcccg cggacgtca cccccagtg gtgctggctc 150

ctgggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200

gtgcactacc tctgtccaa gaagaccgaa agctacttca caatctggt 250

gaacctggaa ctgtctctgc ctgtcatcat tgactgtctgg attgacaata 300

tcaggcttgt ttacaacaaa acatccaggg ccacccagtt tctgatgggt 350

gtggatgtac gtgtccctgg ctttgggaag acctctctac tggagttcct 400

ggaccccagc aaaagcagcg tgggttcta ttccacacc atggtggaga 450

gccttggtgg ctggggctac acacggggtg aggatgtccg aggggtccc 500

tatgactggc gcgagcccc aaatgaaaac gggccctact tctggccct 550

ccgcgagatg atcgagaga tgtaccagct gtatgggggc ccctgggtgc 600

tggttgccc cagtatggc aacatgtaca cgtctactt tctgcagcgg 650

cagccgcagg cctggaagga caagtatc cgggccttcg tgtaactggg 700

tgcgcctgg gggggcgtg ccaagacct ggggtcttg gcttcaggag 750

acaacaacc gatccagtc atcgggccc tgaagatccg ggagcagcag 800

cggtcagctg tctccaccag ctggctgtg cctacaact acacatggtc 850

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actaccgcaa gttcttcag gacatcggt ttgaagatgg ctggctcatg 950

cggcaggaca cagaagggt ggtggaagcc acgatgccac ctggcgtgca 1000

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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu Leu	
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu	Lys Val Phe Val Gln Thr	
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe Gln	
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr Glu	
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro	Gly Val Gln Leu His Cys	
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr Glu	
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly Asp	
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp Gln	
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu	Gln Glu Leu Pro Gly Ser	
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr Leu	
395	400	405
Lys Arg Val Leu Leu Gly Pro		
410		

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctgggggtac acacgggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gcacccaaatg aaaacgggcc ctacttcctg gccctccgag agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
cgagcgcgtg ggccgacgag tggggcggcg gcagcggcgg cgaaggcgac 50
atggagagcg gggcctacgg cgcggccaag gcgggcggct ccttcgacct 100
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 tctcattcaa ag 1512

<210> 162
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 162
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 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala
 20 25 30
 Val Cys Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly
 35 40 45
 Glu Gly Tyr Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val
 50 55 60
 Phe Asn Arg Asn Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly
 65 70 75
 Val Leu Ala Phe Leu Ala Ser Ala Phe Phe Leu Val Val Asp Ala
 80 85 90
 Tyr Phe Pro Gln Ile Ser Asn Ala Thr Asp Arg Lys Tyr Leu Val
 95 100 105
 Ile Gly Asp Leu Leu Phe Ser Ala Leu Trp Thr Phe Leu Trp Phe
 110 115 120
 Val Gly Phe Cys Phe Leu Thr Asn Gln Trp Ala Val Thr Asn Pro
 125 130 135
 Lys Asp Val Leu Val Gly Ala Asp Ser Val Arg Ala Ala Ile Thr
 140 145 150

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu
155 160 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn
170 175 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr
185 190 195

Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln
200 205 210

Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr
215 220

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

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<400> 164

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<213> Homo sapiens

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<210> 169

<211> 802

<212> PRT

<213> Homo sapiens

<400> 169

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Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val
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Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly
			50						55					60
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val
			65						70					75
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe
			80						85					90
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu

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Arg Leu Gly Thr Tyr Tyr Asn Ser Ser	Ser Val Tyr Ser Phe Gly	
125	130	135
Glu Gly Pro Leu Thr Cys Phe Phe Trp	Phe Ile Leu Gln Ile Pro	
140	145	150
Glu His Arg Arg Leu Met Leu Ser Pro	Glu Val Val Gln Ala Leu	
155	160	165
Leu Val Glu Glu Leu Leu Ser Thr Val	Asn Ser Ser Ala Ala Val	
170	175	180
Pro Tyr Arg Ala Glu Tyr Glu Val Asp	Pro Glu Gly Leu Val Ile	
185	190	195
Leu Glu Ala Ser Val Lys Asp Ile Ala	Ala Leu Asn Ser Thr Leu	
200	205	210
Gly Cys Tyr Arg Tyr Ser Tyr Val Gly	Gln Gly Gln Val Leu Arg	
215	220	225
Leu Lys Gly Pro Asp His Leu Ala Ser	Ser Cys Leu Trp His Leu	
230	235	240
Gln Gly Pro Lys Asp Leu Met Leu Lys	Leu Arg Leu Glu Trp Thr	
245	250	255
Leu Ala Glu Cys Arg Asp Arg Leu Ala	Met Tyr Asp Val Ala Gly	
260	265	270
Pro Leu Glu Lys Arg Leu Ile Thr Ser	Val Tyr Gly Cys Ser Arg	
275	280	285
Gln Glu Pro Val Val Glu Val Leu Ala	Ser Gly Ala Ile Met Ala	
290	295	300
Val Val Trp Lys Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe Val	
305	310	315
Leu Ser Val Gln Pro Val Val Phe Gln	Ala Cys Glu Val Asn Leu	
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Thr Leu Asp Asn Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr Pro	
335	340	345
Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp His	
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Leu Thr Val Pro Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe Asp	
365	370	375
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr Gln	

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Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly					
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Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro					
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Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys					
				455					460					465					
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys					
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Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile					
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Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly					
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Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe					
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Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro					
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Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu					
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Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp					
				590					595					600					
Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met					
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Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln					
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Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu					
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Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val					
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Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val					

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680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly		
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro		
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg		
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln		
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg		
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg		
770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser		
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<211> 1327

<212> DNA

<213> Homo sapiens

<400> 170

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 171

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<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

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<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

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<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

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				20					25					30
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
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Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
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Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
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Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
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290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg
320 325 330

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335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro
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<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

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<211> 26

<212> DNA

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<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 181

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<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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 ggtctggaca ctccatcctt gccaaacctc taccctaaag tggccttaag 3050
 caccggaatg ccaattaact agagacctc cagcccccaa ggggaggatt 3100
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
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 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1	5	10	15
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr			

185	190	195
Leu Glu Asp Phe Tyr Gly Val Phe Ser Ser Pro Gly Tyr Thr His		
200	205	210
Leu Ala Ser Val Ser His Pro Gln Ser Cys His Trp Leu Leu Asp		
215	220	225
Pro His Asp Gly Arg Arg Leu Ala Val Arg Phe Thr Ala Leu Asp		
230	235	240
Leu Gly Phe Gly Asp Ala Val His Val Tyr Asp Gly Pro Gly Pro		
245	250	255
Pro Glu Ser Ser Arg Leu Leu Arg Ser Leu Thr His Phe Ser Asn		
260	265	270
Gly Lys Ala Val Thr Val Glu Thr Leu Ser Gly Gln Ala Val Val		
275	280	285
Ser Tyr His Thr Val Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala		
290	295	300
Thr Tyr His Val Arg Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys		
305	310	315
Gly Leu Gly Ser Gly Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg		
320	325	330
Cys Tyr Ser Glu Ala Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala		
335	340	345
Asp Gly Thr Asp Glu Glu Asp Cys Pro Gly Cys Pro Pro Gly His		
350	355	360
Phe Pro Cys Gly Ala Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr		
365	370	375
Leu Pro Ala Asp Arg Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly		
380	385	390
Ala Asp Glu Arg Arg Cys Arg His Cys Gln Pro Gly Asn Phe Arg		
395	400	405
Cys Arg Asp Glu Lys Cys Val Tyr Glu Thr Trp Val Cys Asp Gly		
410	415	420
Gln Pro Asp Cys Ala Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr		
425	430	435
Val Leu Pro Arg Lys Val Ile Thr Ala Ala Val Ile Gly Ser Leu		
440	445	450
Val Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr Cys Lys		
455	460	465
Leu Tyr Ala Ile Arg Thr Gln Glu Tyr Ser Ile Phe Ala Pro Leu		

470	475	480
Ser Arg Met Glu Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro Ser	
485	490	495
Tyr Gly Gln Leu Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu Asp	
500	505	510
Phe Pro Thr Glu Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn Leu	
515	520	525
Arg Ser Leu Leu Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly Gly	
530	535	540
Gly Pro Gly Ala Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg Arg	
545	550	555
Leu Val Arg Arg Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr Asn	
560	565	570
Thr Pro Ala Arg Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro Ser	
575	580	585
Ala Ala Pro Leu Glu Ala Leu Asp Gly	Gly Thr Gly Pro Ala Arg	
590	595	600
Glu Gly Gly Ala Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro Pro	
605	610	615
Leu Pro Ile Lys Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro Ala	
620	625	630
Pro Thr Thr Val Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu Pro	
635	640	645
Leu Glu Pro Ser Leu Leu Ser Gly Val	Val Gln Ala Leu Arg Gly	
650	655	660
Arg Leu Leu Pro Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser Pro	
665	670	675
Pro Gly Pro His Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp Asp	
680	685	690
Val Leu Leu Val Pro Leu Ala Glu Pro	Gly Val Trp Val Ala Glu	
695	700	705
Ala Glu Asp Glu Pro Leu Leu Thr		
710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca etc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgcctgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
gggtattgct tgccttgga cagacctgt ggcttaggt ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggg gctccgccgc ggtggcggtt 50
gtatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgtctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150
 aataaaacat cgcctcttct gcttcagtgt gaaaggccac gtgaagatgc 200
 tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450
 agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550
 cagaaaaagc ctgtgcatga aaaaaagaa gttttgtaat tttatattac 600
 ttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
 aaaaaaaaaa aaa 663

<210> 190
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe
 1 5 10 15
 Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val
 20 25 30
 Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr
 35 40 45
 Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile
 50 55 60
 Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe
 65 70 75
 Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe
 80 85 90
 Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
 95 100 105
 Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys
 110 115 120
 Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn
 125 130 135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
140 145 150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
catgccccct tctgtttcag tgtgaaaggc cacgtgaaga tgcctgggct 200
ggcactaact gngacatcta tgaccttttt tatnatcgca caagccccctg 250
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
gcctttgctt gatattatca actcactggg aacaacagta ttcattgetca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193

ctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtctg tgtgtgggtct gcagacgga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccggc cgcgggcga gtcgtgagc cgcggctgcc ggaagggaacg 50

ggaacggcta ggtctgggcg cccccggg ccccgccgtg ggcattggcg 100

caatggcccg ggcgtgtctg ctgcctctgc tggccagtg gctctgcgc 150

gcgcgcccg agctggccc cgcgccttc acgtgcccc ccgggtggc 200

cggggccacg aacggcgtag ttgcgcacc cccgggaccc gggacccctg 250

ccgagcgcca cgcgcacggc ttggcgtctg cctggagcc tgcctggcg 300

ccccccggg gcgcgcaca cttcttggc atggtagaca acctgcagg 350

ggaactctgc cgcggctact acctggagat gctgatggg accccccgc 400

agaagetaca gattctcgtt gacactggaa gcagtaactt tgcctggca 450

ggaacccgc actctacat agacacgtac ttgacacag agaggtctag 500

cacataccgc tccaagggt ttgacgtac agtgaagtac acacaaggaa 550

gctggacggg ctctgttgg gaagacctg tcaccatccc caaaggcttc 600

aatacttctt ttctgtcaa cattgcact atttttgaat cagagaattt 650

ctttttgcct gggattaaat ggaatggaat acttggccta gtttatgcca 700

caattgcaa gccatcaagt tctctggaga ccttcttoga ctccctggtg 750

acacaagcaa acatcccaa cgttttctcc atgcagatgt gtggagcccg 800

cttgccggtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850

gaattgaacc aagtttgtat aaaggagaca tctggtatac cctattaag 900

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acatttccag ggcagcagcc gggatcgatg gtggcgcttt ctctgtgcc 1750
caccgctctt caatctctgt tctgtccca gatgccttct agattcactg 1800
tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850
aaataattaa aaaaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT.

<213> Homo sapien

<400> 196

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Gln
1				5					10				15	

Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
			20					25					30	

Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
			35					40					45	

Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
			50					55					60	

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala		65	70	75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg		80	85	90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu		95	100	105
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly		110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser		125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr		140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile		155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile		170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly		185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser		200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro		215	220	225
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala		230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu		245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu		260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly		275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala		290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val		305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro		320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp		335	340	345

Thr Asn Ser Glu Thr Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile	350	355	360
Tyr Leu Arg Asp Glu Asn Ser Ser Arg Ser Phe Arg Ile Thr Ile	365	370	375
Leu Pro Gln Leu Tyr Ile Gln Pro Met Met Gly Ala Gly Leu Asn	380	385	390
Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro Ser Thr Asn Ala Leu	395	400	405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp	410	415	420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu	425	430	435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr	440	445	450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu	455	460	465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly	470	475	480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg	485	490	495
Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser	500	505	510
Ser Leu Val Arg His Arg Trp Lys	515		

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

gcgagaagct acagattctc g 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19

<210> 199
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 199
ggatgtagcc agcaactgtg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gacttggtc gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggtcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagaacta cctcogttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204

<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA
<213> Homo sapiens

<400> 205
cgctctccgcc ttccgaggct gaacgcgccg ggcgcggttc caggcctgtg 50
caggggcggat cggcagccgc ctggcggcga tccagggcgg tgcggggcct 100
gggcgggagc cgggagggcg ggcgcgcgat gaggcgctgc tgcctgggcg 150
gggggttgcgt ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200
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<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30
Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45
Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60
Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala Ala Phe Asp	Leu Arg Gln Glu Ser	Gly Asn Asn Glu Val	Ile
	80	85	90
Phe Met Ala Leu Asp	Leu Ala Ser Leu	Ala Ser Val Arg Ala	Phe
	95	100	105
Ala Thr Ala Phe	Leu Ser Ser Glu Pro	Arg Leu Asp Ile Leu	Ile
	110	115	120
His Asn Ala Gly	Ile Ser Ser Cys Gly	Arg Thr Arg Glu Ala	Phe
	125	130	135
Asn Leu Leu Leu	Arg Val Asn His Ile	Gly Pro Phe Leu Leu	Thr
	140	145	150
His Leu Leu Leu	Pro Cys Leu Lys Ala	Cys Ala Pro Ser Arg	Val
	155	160	165
Val Val Val Ala	Ser Ala Ala His Cys	Arg Gly Arg Leu Asp	Phe
	170	175	180
Lys Arg Leu Asp	Arg Pro Val Val Gly	Trp Arg Gln Glu Leu	Arg
	185	190	195
Ala Tyr Ala Asp	Thr Lys Leu Ala Asn	Val Leu Phe Ala Arg	Glu
	200	205	210
Leu Ala Asn Gln	Leu Glu Ala Thr Gly	Val Thr Cys Tyr Ala	Ala
	215	220	225
His Pro Gly Pro	Val Asn Ser Glu Leu	Phe Leu Arg His Val	Pro
	230	235	240
Gly Trp Leu Arg	Pro Leu Leu Arg Pro	Leu Ala Trp Leu Val	Leu
	245	250	255
Arg Ala Pro Arg	Gly Gly Ala Gln Thr	Pro Leu Tyr Cys Ala	Leu
	260	265	270
Gln Glu Gly Ile	Glu Pro Leu Ser Gly	Arg Tyr Phe Ala Asn	Cys
	275	280	285
His Val Glu Glu	Val Pro Pro Ala Ala	Arg Asp Asp Arg Ala	Ala
	290	295	300
His Arg Leu Trp	Glu Ala Ser Lys Arg	Leu Ala Gly Leu Gly	Pro
	305	310	315
Gly Glu Asp Ala	Glu Pro Asp Glu Asp	Pro Gln Ser Glu Asp	Ser
	320	325	330
Glu Ala Pro Ser	Ser Leu Ser Thr Pro	His Pro Glu Glu Pro	Thr
	335	340	345
Val Ser Gln Pro	Tyr Pro Ser Pro Gln	Ser Ser Pro Asp Leu	Ser
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Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
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Leu Ser

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

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<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

acgccagtgg cctcaagctg gttg 24

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<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 3716

<212> DNA

<213> Homo sapiens

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caagcctcag gccagccacc tcccaccatc cgttggttgc tgaatgggca 200

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 <213> Homo sapiens

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 20 25 30
 Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu
 35 40 45
 Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu
 50 55 60
 Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly
 65 70 75
 His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
 80 85 90
 Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly
 95 100 105
 Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln
 110 115 120
 Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu
 125 130 135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met	Glu	Arg	Ala	Thr	Gln	Glu	Pro	Ser	Glu	His	Gly	Pro	Trp	Thr	425	430	435
Leu	Glu	Gln	Leu	Arg	Ala	Thr	Leu	Lys	Arg	Pro	Glu	Val	Ile	Ala	440	445	450
Thr	Cys	Gly	Val	Ala	Leu	Trp	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Val	455	460	465
Cys	Ile	His	Arg	Arg	Arg	Arg	Ala	Arg	Val	His	Leu	Gly	Pro	Gly	470	475	480
Leu	Tyr	Arg	Tyr	Thr	Ser	Glu	Asp	Ala	Ile	Leu	Lys	His	Arg	Met	485	490	495
Asp	His	Ser	Asp	Ser	Gln	Trp	Leu	Ala	Asp	Thr	Trp	Arg	Ser	Thr	500	505	510
Ser	Gly	Ser	Arg	Asp	Leu	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Arg	515	520	525
Leu	Gly	Ala	Asp	Ala	Arg	Asp	Pro	Leu	Asp	Cys	Arg	Arg	Ser	Leu	530	535	540
Leu	Ser	Trp	Asp	Ser	Arg	Ser	Pro	Gly	Val	Pro	Leu	Leu	Pro	Asp	545	550	555
Thr	Ser	Thr	Phe	Tyr	Gly	Ser	Leu	Ile	Ala	Glu	Leu	Pro	Ser	Ser	560	565	570
Thr	Pro	Ala	Arg	Pro	Ser	Pro	Gln	Val	Pro	Ala	Val	Arg	Arg	Leu	575	580	585
Pro	Pro	Gln	Leu	Ala	Gln	Leu	Ser	Ser	Pro	Cys	Ser	Ser	Ser	Asp	590	595	600
Ser	Leu	Cys	Ser	Arg	Arg	Gly	Leu	Ser	Ser	Pro	Arg	Leu	Ser	Leu	605	610	615
Ala	Pro	Ala	Glu	Ala	Trp	Lys	Ala	Lys	Lys	Lys	Gln	Glu	Leu	Gln	620	625	630
His	Ala	Asn	Ser	Ser	Pro	Leu	Leu	Arg	Gly	Ser	His	Ser	Leu	Glu	635	640	645
Leu	Arg	Ala	Cys	Glu	Leu	Gly	Asn	Arg	Gly	Ser	Lys	Asn	Leu	Ser	650	655	660
Gln	Ser	Pro	Gly	Ala	Val	Pro	Gln	Ala	Leu	Val	Ala	Trp	Arg	Ala	665	670	675
Leu	Gly	Pro	Lys	Leu	Leu	Ser	Ser	Ser	Asn	Glu	Leu	Val	Thr	Arg	680	685	690
His	Leu	Pro	Pro	Ala	Pro	Leu	Phe	Pro	His	Glu	Thr	Pro	Pro	Thr	695	700	705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 212
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<220>
<223> Synthetic oligonucleotide probe

<400> 213
actgaccttc cagctgagcc acac 24

<210> 214
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

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<212> DNA
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<222> 1869, 1887
<223> unknown base

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 tttgtgtac ttccttcac tcttttctc ttcacataat ttgccggtgt 2600
 tctttttaca gagcaattat cttgtatata caactttgta tcttgccctt 2650
 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
1				5				10					15	

Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
				20					25					30

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
				35					40					45

His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	50		55		60
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met	65		70		75
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu	80		85		90
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr	95		100		105
Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile	110		115		120
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser	125		130		135
Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala	140		145		150
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu	155		160		165
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu	170		175		180
Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr	185		190		195
Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro	200		205		210
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala	215		220		225
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg	230		235		240
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu	245		250		255
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His	260		265		270
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln	275		280		285
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys	290		295		300
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro	305		310		315
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val	320		325		330

Ser Ala

<210> 217
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 217
ccctgcagtg cacctacagg gaag 24

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 218
ctgtcttccc ctgcttggct gtgg 24

<210> 219
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 219
ggcgcaggaa gggcgggac ctctctctc gctgctctg ccacac 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
ttgtgactaa aagctggcct agcaggccag ggagtgacgc tgcaggcgtg 50
gggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100
cagtgtgaaa gaaccagtgg tctcgtctg ttgccaggc tagagtgtac 150
tggcgtgac atagctcact gcagcctcag actcctggac ttgagaaatc 200
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
cctgtttctt ctctctctgt gagtggacca cggaggctgg tgagctgcct 300
gtcatcccaa agctcagctc tgagccagag tggcggcggc tccacctctg 350
ccgcggcat agaagccagg agcagggtc tcagaaggcg gtggtgcca 400

gctgggatca tgttgttggc cctgggtctgt ctgctcagct gcttgctacc 450
ctccagttag gccaaactct acgggtcgttg tgaactggcc agagtgtac 500
atgacttcgg gctggacgga tacgggggat acagcctggc tgactgggtc 550
tgcccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
ggtgcagcaa cctcaccocg aacgtcccca acgtgtgccg gatgtactgc 700
tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
gatggacgga accatgcaca gcaggctggg aaatgtgggt tggttcctga 900
cctaggcttg ggaagacaag ccagcgaata aaggatgggt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser	1	5	10	15
Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu	20	25	30	
His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp	35	40	45	
Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala	50	55	60	
Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln	65	70	75	
Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro	80	85	90	
Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu	95	100	105	
Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln	110	115	120	
Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys	125	130	135	
Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe	140	145						

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
gggatcatgt tggtggccct ggtc 24

<210> 223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gcaaggcaga ccagtcagc cag 23

<210> 224
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgectgcta cctccaagt gaggccaagc tatacggteg ttgtg 45

<210> 225
<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccgggccggg cgcgcgcggc ggcaccatga gtccccgctc 50
gtgectgggt tgctgcgcc tctcgtctt cgcctcttc tcagccgccg 100
cgagcaactg gctgtacctg gccaaactgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctcgggtgcgc cgcgggtgcc 250
agctggccat tgaggagtgc cagtaaccagt tcgggaaccg gcgctggaac 300
tgctccacac tcgactcctt gcccgctcttc ggcaagggtgg tgacgcaagg 350
gactcgggag ggggccttcg tgtacgccat ctcttcggca ggtgtggcct 400
ttgcagtjac gggggcgtgc agcagtgggg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500
ctctgacaac atcgccctacg gtgtggcctt ctccagtcg tttgtggatg 550
tgccgggagag aagcaagggg gcctcgcca gcagagccct catgaacctc 600
cacaacaatg aggcggcag gaaggccatc ctgacacaca tgcgggtgga 650
atgcaagtgc caggggtgt caggctcctg tgaggtaaag acgtgctggc 700
gagccgtgcc gcccttcgc cagggtgggc acgcactgaa ggagaagttt 750
gatggtgcca ctgaggtgga gccacggcg gtgggtcct ccagggcact 800
ggtaccacgc aagccacagt tcaagccga cacagatgag gacctggtgt 850
acttgagcc tagcccgac ttctgtgagc aggacatgc cagcggcgtg 900
ctgggcacga ggggcgcac atgcaacaag acgtccaagg ccacgacgg 950
ctgtgagctg ctgtgctgtg gccggcgtt ccacacggcg cagggtgagc 1000
tggtgaaag ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050
cggcagtgc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100
ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150
aaacagtctc ccaccacctc cccaagaga tactggtgt atttttgtt 1200
ctgggttggg tttgggtcc tcattgtatt tattgcgaa accaggcagg 1250
caaccccaag ggcaccaacc agggcctccc caaagcctgg gcccttgtgg 1300
ctgccactga ccaaagggac ctgtcctgt ccgctggctg ccgcatgtg 1350
gtgccactg accactcagt tgttatctgt gtccgttttt ctacttgag 1400
acctaaagtg gagtaacaag gattattacc accacatggc tactgacct 1450
gtccatcggtg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500
atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550
tacacatgga ctctggcag cttgagccta gaagccatgt ctctcaaatg 1600
ccctgagaaa ggaacaagc agataccagg tcaagggcac caggttcatt 1650
tcagccctta catggacagc tagaggttcg atatctgtgg gtccctccag 1700
gcaagaagag ggagatgaga gcaagagag actgaagtc caccctagaa 1750
cccagcctgc ccagcctgc ccctgggaag aggaaactta accactccc 1800
agaccacct aggcaggcat ataggctgc atcctggacc agggatccc 1850

gctgtgcctt tgcagtcatg cccgagtcac ctttcacagc gctgttcctc 1900
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000
ctgtgccttt gcagtcatgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
1				5					10					15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
				20					25					30
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
				35					40					45
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn
				50					55					60
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile
				65					70					75
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser
				80					85					90
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly
				95					100					105
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val
				110					115					120
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro

215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly		
230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu		
245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu		
260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg		
275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser		
290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe		
305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe		
320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val		
335	340	345
Glu Leu His Thr Cys Arg		
350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gotgcagctg caaattccac tgg 23

<210> 228

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 228

tggtagggaga ctgtttaaat tatcggcc 28

<210> 229

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctggaggt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

cggaacgctg ggccgacggg tggcgaggag cgtggggcga cgcgtgggct 50
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100
gtcccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgagg 250
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
ggggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450
cgcgtagacc agggcttggc tgaagccggc agggggcgtg aggacgtccg 500
cactgagctg ttccgggcgc tggaggccgt gaggtccag aacaactcct 550
ggagacgctg cccacgctg tggctgtcct tcgagggctc ctgctacttt 600
ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650
tgccagcgcg cacttggtga tcgttggggg cctggatgag cagggttcc 700
tcaactcgaa cagcgtggc cgtggttact ggctgggcct gagggtgtg 750
cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
gacagcgaga aggaaggctg gatctgtgag aaaaggcaca actgctgacc 950
ccggccagtg ccctggagcc gcgcacattg cagcatgtcg tatcctgggg 1000
gtgtctcacc tccctggctc ctggagctga ttgccaaaga gtttttttct 1050
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tgtccagccc agtgccctgg ctctgggacc tccatgccga cctcctccta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
 ctctgcgctc cccgtgatat gcctccactt ctctccctaa ccaagggttag 1250
 gtgactgagg actggagctg ttgggttttc tgcattttc caccaaactg 1300
 gaagctgttt ttgcagcctg aggaagcacc aataaatatt tgagaaatga 1350
 aaaaa 1355

<210> 231
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 231
 Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu
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 Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
 20 25 30
 Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
 35 40 45
 Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
 50 55 60
 Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
 65 70 75
 Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
 80 85 90
 Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
 95 100 105
 Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
 110 115 120
 Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
 125 130 135
 Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg
 140 145 150
 Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys
 155 160 165
 Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser
 170 175 180
 Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp
 185 190 195
 Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly
 200 205 210

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp
275 280 285

Ile Cys Glu Lys Arg His Asn Cys
290

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

jcgagaaatg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caacgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gaggtgata cgacccggg aaggtogctg ggcagggcga 50
gttgggaaag cggcagcccc cgccgcccc gcagccctt ctctctctt 100
ctcccacgtc ctatctgct ctogctggag gccaggcctg gcagcatcga 150
agacaggagg aactggagcc tcattggccg gcccgggcg ccggcctcgg 200
gcttaaatag gagctccggg ctctggctgg gaccgaccc ctgcggcgc 250
cgctcccgct gctctgccc ggtgatggaa aaccccagcc cggccgcgc 300
cctgggcaag gccctctgcg ctctctctt ggacactct ggccgcgcgc 350
gccagcctct tgggggagag tccatctgtt ccgcagagc ccgggcaaaa 400
tacagatca ccttcacggg caagtggagc cagacggcct tccccagca 450
gtacccctg ttccgcccc ctgcgcagtg gtcttctctg ctgggggcgc 500
cgcatagtc cgactacagc atgtggaggc agaaccagta cgtcagtaac 550
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cagcgcaggc actcgttgt ctgtttgtg gtgcgcctc tgcccagccc 750
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cggagccatg ggggtgcggg ggctcctgt caggctcatg ctgcaggcgg 1350
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cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
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 cagctactct aaattatgtc tcttataag ttattgctgc tccaggagat 1600
 tgtcttcat cgtccagggg cctggctccc acgtggttgc agatacctca 1650
 gacctggtgc tctaggctgt gctgagccca ctctccgag ggcgcaccca 1700
 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750
 gtgtttccat gttatggatc tctctggtt tgaataaaga ctatctctgt 1800
 tgcacacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys
 1 5 10 15
 Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly
 20 25 30
 Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile
 35 40 45
 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr
 50 55 60
 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala
 65 70 75
 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val
 80 85 90
 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala
 95 100 105
 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val
 110 115 120
 His Glu Val Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln
 125 130 135
 Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His Ser Leu Val Ser
 140 145 150
 Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe Val Gly Val
 155 160 165

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala	170	175	180
Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe	185	190	195
Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val	200	205	210
Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe	215	220	225
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr	230	235	240
Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala	245	250	255
Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser	260	265	270
Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser	275	280	285
Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser	290	295	300
Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro	305	310	315
Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys	320	325	330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcaatgcc aggggaagag gg 22

<210> 238

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagcccttc tctccttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtctgcggg atg 23

<210> 243
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
cagcccttc tctccttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

ggcggcgctcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50
tgtcttgctg gatattgaca aactgaagct ttctgcacc actggactta 100
aggaagagtg tactcgtagg cggacagctt tagtggccgg cgggccgctc 150
tcaccccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc cttaaagcttg 300
cagaaatttt atccaacttt gtttggaagc ttattatgac aataccattt 350
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tctactggc 400
acagggagtg gtggagagtc tatctatgga gcgcattca aagatgaatt 450
tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaatg 500
ctggttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550
gatgaactta acaataagca taccatcttt ggaaagggtta caggggatac 600
agtatataac atgttgcgac tgcagaagt agacattgat gatgacgaaa 650
gaccacataa tccacacaaa ataaaaagct gtgaggtttt gtttaatcct 700
tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750
agaggaggaa gttaaagaaat tgaaacccaa aggcacaaaa aatttttagtt 800
tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaatacga 850
gttagtcaga gcatgaaggg caaaagcaaa agtagtcatg acttgcttaa 900
ggatgatcca catctcagtt ctgttcagt tgtagaaagt gaaaaagggtg 950
atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000
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aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150
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tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gccctccag 1250
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aggaagcaac agtcaaagaa gggaacttcc cggaagatc agacccttgc 1350
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 ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450
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 catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550
 ataaaagaag gaggggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600
 agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650
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 gaaaagaagt atttttgaac ctgttgctg gttttgaaaa acaattatct 1750
 tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800
 catgtgtttt ttctagctg accttttata ttgctaaatc tgaaataaaa 1850
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 245
 Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val
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 Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser
 20 25 30
 Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu
 35 40 45
 Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly
 50 55 60
 Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly
 65 70 75
 Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg
 80 85 90
 Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly
 95 100 105
 Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala
 110 115 120
 Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly
 125 130 135

Asp Thr Val Tyr	Asn Met Leu Arg Leu	Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg	Pro His Asn Pro His	Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn	Pro Phe Asp Asp Ile	Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys	Glu Lys Pro Glu Glu	Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr	Lys Asn Phe Ser Leu	Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu	Glu Glu Glu Val Asn	Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser	Lys Ser Ser His Asp	Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser	Val Pro Val Val Glu	Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val	Asp Asp Gly Glu Asp	Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp	Gly Asp Glu Lys Asn	Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu	Lys Lys Asp Thr Ser	Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu	Val Glu Lys Lys Ser	Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu	Ala Arg Gln Leu Lys	Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys	Val Glu Asn Ala Ala	Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu	Glu Ala Pro Pro Asp	Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys	Gln Lys Tyr Glu Ala	Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr	Ser Arg Glu Asp Gln	Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser	Lys Leu Thr Gln Ala	Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro	Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met
455 460 465

Arg Glu Lys Lys Glu Arg Arg
470

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tggtgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
ctgggttcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 252
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
cgccgcggtt ggggctggaa gttcccgcca ggtccgtgcc gggcgagaga 50
gatgctgccc ggccgcctc ggctttgagg cgagagaagt gtccagacc 100
catttcgcct tgetgacggc gtcgagccct ggccagacat gtccacaggg 150
ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200
gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250
cttctgtggg gctcaatatt ggaaatcttg gaagtacttc aactccagca 300
actacatctg ctcttcaag tggttttgga accgggctct ttggatctaa 350
acctgccact gggttcactc taggaggaac aaatacagg gtcttgaca 400
ccaagaggcc tcaagtgtc accaaatatg gaacctgca aggaaaacag 450
atgcatgtgg ggaagacacc catccaagtc tttttaggag tccccttctc 500

cagacctcct ctaggtatcc tcaggtttgc acctccagaa cccccggagc 550
cctggaaagg aatcagagat gctaccacct acccgctgg atggagtctc 600
gctctgtcgc caggctggag tgcagtggca cgatctcggc tcaactgcaac 650
ctccgcctcc cgggttcaag cgagtctcct gctcagcct ctgagtgtct 700
ggggctacag gtgcctgcag gagtccctggg gccagctggc ctgatgtac 750
gtcagcacgc gggaaacggta caagtggctg cgttccagcg aggactgtct 800
gtacctgaac gtgtacgcgc cggcgcgcgc gcccggggat cccagctgc 850
cagtgatggt ctggtccccg ggaggcgctt tcctcgtggg cgtgcttct 900
tcgtacgagg gctctgactt ggccgcgcgc gagaaagtgg tgotggtgtt 950
tctgcagcac aggtcgggca tcttcggtt cctgagcacg gacgacagcc 1000
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accacttggt gtggaggagt acctggacaa tgtcaatgag catgaactgga 1600
agatgctacg aaacctatg atggacatag ttcaagatgc cactttcgtg 1650
tatgccacac tgcagactgc tcactaccac cgagaaacc caatgatggg 1700
aatctgcctt gctggccacg ctacaacaag gatgaaaagt acctgcagct 1750
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tttgatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850
taagggtggc tatgcaggaa ggagccaaag aggggtttgc cccaccatc 1900

caggccctgg ggagactagc catggacata cctggggaca agagttctac 1950
 ccaccccagt ttagaactgc aggagctccc tgctgcctcc aggccaaagc 2000
 tagagctttt gcctgtttg tgggacctgc actgcccttt ccagcctgac 2050
 atcccatgat gcccctctac ttactgttg acatccagtt aggccaggcc 2100
 ctgtcaacac cacactgtgc tcagctctcc agcctcagga caacctcttt 2150
 ttttcccttc ttcaaactcc cccacccttc aatgtctcct tgtgactcct 2200
 tcttatggga ggtcgaccca gactgccact gccctgtca ctgcacccag 2250
 cttggcattt accatccatc ctgtcaacc ttgttctgt ctgttcacat 2300
 tggcctggag gctagggca ggtgtgaca tggagcaaac ttttggtagt 2350
 ttgggatctt ctctccacc cacacttacc tccccaggg ccactccaaa 2400
 gtctatacac aggggtggtc tcttcaataa agaagtgttg attagaaaaa 2450
 aaaaaa 2456

<210> 254
 <211> 545
 <212> PRT
 <213> Homo sapiens

<400> 254
 Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr
 1 5 10 15
 Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe
 20 25 30
 Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
 35 40 45
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
 50 55 60
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
 65 70 75
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
 80 85 90
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
 95 100 105
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
 110 115 120
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
 125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	140	145	150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro		
	425	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu		
	440	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn		
	455	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp		
	470	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met		
	485	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr		
	500	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala		
	515	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu		
	530	540
Pro Gln Glu Trp Ala		
	545	

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

agggtgactgc aggagtactg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

gaacgggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

gagaaaggc ctgtctcagg caggccctgc gctcctatg cggagatgct 50

actgccactg ctgctgtcct cgtctgtggg cgggtcccag gctatggatg 100

ggagattctg gatacagtg caggagtcag tgatgggtgcc ggagggcctg 150

tgcattctctg tgcctgtctc ttctcctac ccccgacaag actggacagg 200

gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250

agggtgctcc tgtggccaca aaccaccaga gtccagaggt ggaaatgagc 300

accgggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350

cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400

gggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450

tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500

caccgacctc acctgccatg tggacttctc cagaaagggg gtgagcgcac 550

agaggacctg ccgactcctg gtggcctatg ccccagaga ccttgttatc 600

agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaag 650

tgtccatac ctggaagccc aaaaaggcca gttcctgcgg ctctctctgtg 700

ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750

gtcctctcct cgtcccatcc ctggggccct agaccctgg ggctggagct 800

gcccgggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850

acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900

ccagagaacc tgagagtgat ggttttccaa gcaaacagga cagtccctgga 950

aaaccttggg aacggcacgt ctctccagct actggagggc caaagcctgt 1000

gcttggtctg tgtcacacac agcagccccc cagccaggt gagctggacc 1050

cagaggggac aggttctgag cccctccag cctccagacc ccggggctcct 1100

ggagctgcct cgggttcaag tggagcacga aggagagttc acctgccacg 1150

ctgggaccc actgggtccc cagcacgtct ctctcagcct ctccgtgcac 1200

tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250
aatcggcatac acggtctctc ttttctctg cctggccctg atcatcatga 1300
agattctacc gaagagacgg actcagacag aaaccccgag gccaggttc 1350
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ctgggaactc ggctaggag gaaggtagag taagagggtg aagataacag 1750
agtgc aaagt ttcctctct cctctctct ctctctctct 1800
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tggggagtcc gagaccagcc tggccaaact ggtgaaacc cgtctctact 1950
aaaaatacaa aaattagctg ggcattggtg caggcgctg taactctacc 2000
taattgggaa gctgaggcag gagaatcact tgaacctggg agacggaggt 2050
tgcagtgage caagatcaca ccattgcaag ccagcctggg caacaaagg 2100
agactccatc tcaaaaaaaaa atcctccaa atgggttggg tgtctgtaat 2150
ccagcactt tgggaggcta aggtgggtg attgcttgag ccaggaggt 2200
cgagaccagc ctgggcaaca tggtgaaacc ccatctctac aaaaaatata 2250
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tttaaaccag agcaactcca tctggaatag gagctgaata aatgagggt 2350
gagacctact gggctgcatt ctacagacgt ggaggcattc taagtcaag 2400
gatgagacag gaggtccgta caagatacag gtcataaaga ctttgctgat 2450
aaaacagatt gcagtaaaga agccaaccaa atcccaccaa aaccaagttg 2500
gccacgagag tgacctctg tctctctac tctacactc ctgacagcac 2550
catgacagtt tacaaatgcc atggcaacat cagggaagtt cccgatatgt 2600
cccaaaaggg ggaggaatga ataaccacc ccttgtttag caaataagca 2650

agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700
 ctatggagta gccattcttt tgttccttta ctttcttaat aaacttgctt 2750
 tcaccttaaa aaaa 2764

<210> 259
 <211> 544
 <212> PRT
 <213> Homo sapiens

<400> 259
 Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln
 1 5 10 15
 Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met
 20 25 30
 Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr
 35 40 45
 Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp
 50 55 60
 Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr
 65 70 75
 Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe
 80 85 90
 Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile
 95 100 105
 Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val
 110 115 120
 Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe
 125 130 135
 Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp
 140 145 150
 His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly
 155 160 165
 Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro
 170 175 180
 Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu
 185 190 195
 Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys
 200 205 210
 Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro
 215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
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Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caagagctgc gctggtctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagaggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

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<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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actgctgcgt tttatgttgg gaattctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaac aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

aatgaatacg actagtcac acatcggcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
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 tatgatcata tttgggttta tttttttgac tttgggttta aaacaacgga 1900
 gaaaacagat tctatttctc gagaaaagtg aagatttcag agagaatata 1950
 ttccaatatg atgatgaagg ggggtggagaa gaagatacag aggcctttga 2000
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 aaaccacaag cgtcgagatc aggagcctat acaggcagtc tttgcaagtt 2100
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 aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650
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 atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800
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<210> 264
 <211> 772
 <212> PRT
 <213> Homo sapiens

<400> 264

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Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys	20	25	30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	35	40	45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	50	55	60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Ile	Asp	Asn	Gly	Asn	Asn	65	70	75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	80	85	90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	95	100	105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	110	115	120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	125	130	135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	140	145	150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	155	160	165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	170	175	180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	185	190	195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	200	205	210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	215	220	225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	230	235	240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	245	250	255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	260	265	270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	275	280	285	

Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		290	295	300
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		305	310	315
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		320	325	330
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		335	340	345
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln		350	355	360
Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr		365	370	375
Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly		380	385	390
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg		395	400	405
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly		410	415	420
Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Trp		425	430	435
Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln		440	445	450
Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp		455	460	465
His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu		470	475	480
Asn	Ala	Gly	Ser	Gly	Gln	Val	Ile	Gln	Thr	Ile	Ser	Ala	Val	Asp		485	490	495
Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser		500	505	510
Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln		515	520	525
Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu		530	535	540
Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn		545	550	555
Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val		560	565	570

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	575	580	585
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	590	595	600
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	605	610	615
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	620	625	630
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	635	640	645
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	650	655	660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	665	670	675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	680	685	690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	695	700	705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	710	715	720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	725	730	735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	740	745	750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	755	760	765
Ser	Ala	Val	Gln	Ser	Asn	Asn									770		

<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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gaatatatttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100

attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
aagtgtatta attaaacttt cagatgttaa tgacaataag cctatatatta 200
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg cacc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactaagggt attagagcaa aagttaaaaa ccatcatggt tcttgagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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ccgcgccttaa cttcctccgc ggggcaccgc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg cttctgcac ctgccacccc tgagccagcg 200
cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250
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<210> 270
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 270
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 1 5 10 15
 Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

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Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala	35	40	45
Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly	50	55	60
Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser	65	70	75
Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu	80	85	90
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met	95	100	105
Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val	110	115	120
Ile Gly Gly Ala Ile Phe Leu Leu Ala Gly Leu Ala Ile Leu Val	125	130	135
Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp	140	145	150
Pro Met Thr Pro Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu	155	160	165
Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala	170	175	180
Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr	185	190	195
Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr	200	205	210

Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

<400> 271
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 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt cengcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
 tgatgggtgtt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
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 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
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 gacctatga cccagtc aa tgccagggtac gaatttggtc aggcctctctt 500
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 gctgttctg tccc 564

<210> 272
 <211> 498
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 30, 49, 102, 141, 147, 171, 324-325, 339-341
 <223> unknown base

<400> 272
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 cntcagcaact gccctgcccc agtggaggat ttactcttat nccggnaca 150
 acatcgtgac cgcccaggcc ntgtacgagg ggtgtggat gtctgcgtg 200
 tgcagagca cggggcagat ccagtgc aaa gtctttgact ccttgctga 250
 atctgagtag cacattgcaa gcaaccgtg ccttgatggt ggttggcatc 300
 ctctgggag tgatagcaat cttnttgcc acggttgtnn ntgaagtgt 350
 tgaagtgcctt ggaagacgat gaggtgcaga agatgaggat ggtgtcatt 400
 gggggcgaga tatttcttct tgcaggtctg gctattttag ttgccacagc 450
 atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccga 498

<210> 273
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394

<223> unknown base

<400> 273

gggcccgcacc attatccaac cgggntcact gttggctcat ctccctcctg 50
gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccat 100
gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150
cnjcggtgctg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac ccttgccctg atggtggttg 250
gcctcctcct gggagtata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttggaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgagg tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcggtcaa gaattctatg accctatgac 450
cccagtcaat gccaggtacg aatttggtca ggctctcttc actggctggg 500
ctgctgcttc tctctgcctt ctgggaggtg cctactttg ctgttccctgc 550
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctcccct cctggatgga tcgncacc gtcacattgc ctcccccan 50
tgaggattn actcctatgc tggcgacaac atcgtgacc cccaggccat 100
ttaccgaggg gctttggatg tctgcntgt cgcagagcac cgggcagatc 150
ccagtcaaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
caaccctgct cttgatggg ttggcatcct cctgggagt atagcaacct 250
ttgtggccac cgttggtatg aagtgtatga agtgcttga agacgatgag 300
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgtg 350
caggtctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400
cnngnnntct atgacctat gacccagtc aatgccaggt acgaatttgg 450

tcaggctctc ttcactggct gggetgctgc ttctctctgc cttctgggag 500
gtgccctact ttgctgttcc tgccc 526

<210> 275
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
<223> unknown base

<400> 275
agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50
gcagcacatt ncaagcaacc ccttgcccttg aaggtgggtg ncaccccccc 100
tgggagtgaa tagcaatctt tgtggccacc gttggcatga agtntatgaa 150
gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200
ggcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250
tatggcaata gnatnnttcg nggnttctat gacctatga cccagtcaa 300
tgccaggtac gaatttggtc aggtctctct cactggctgg gctgctgctt 350
ctctctgctt tctgggaggt gccctacttt gctgttcttg tccccgaa 398

<210> 276
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
<223> unknown base

<400> 276
agcaatgccc tgccccagtg ggaggattaa ttcttatgnt ggggacaaca 50
ttgtgaengc ccaggccatg tacggggggc tgtggatgtc ctgcgtgtcg 100
cagagcaccg ggcagatcca gtgcaaagtn ttgactcct tgotgaattt 150
gagcagcaca ttgcaagcaa cccgtgcctt gatgggtggtt ggcatcttcc 200
tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250
tgcttggag acgatgaggt gcagaagatg aggatggctg tcattggggg 300
cgcgatattt ctntttgcag gtctggctat ttagttgcc acagcatggt 350
atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg cctantttg ctgttcttgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

tcacaggggg gcgcgatatt ttttcttgca ggtntgggta ttttagttgc 50

cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

ccccagtcac tgccaggtac gaatttggtc aggcctctntt cactggntgg 150

ctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcttg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

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ttacnctat gctggcgaac aacatctga ccgccaggc catgtaagag 100

gggctgtgga atgtcttgcg tgtccagag caccgggcag atccagtgc 150

aagtctttga ctcttgcg aatctgagca gcacattgca agcaacntg 200

cattgatggt gggtggcatc ctctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtgt tgaagtgtt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgcga tatttctct tgcaggtctg 350

gtatatttag nngccacagc atggatatgc aatcagacc nntcanaaac 400

tatatgacc tatgaccca gtcaatgcca ggtacgaatt tggtcaggct 450

ctcttcaatg gctgggtgc tgttctctc tgccttcttg gaggtgcct 500

actttgtgt tctgttccc gaaaaacaac ctcttaccac cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
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ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100
acaacatcgt gaccnccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgcagag caccgggcag atccagtga aagtctttga ctcttgcgtg 200
aatctgagca gcacattgca agcaacctg ccttgatggg ggttggcatc 250
ctcttgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgcctg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350
ggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgacccag 450
ccaatgccag gtacgaattt ggtcaggctc tcttactgg ctgggctgct 500
gcttctctct gccttctggg aggtgccta ctttgcgtt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgagcgagtc atggccaaag c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtgtcacacg tagtctttcc cgctgg 26

<210> 282
<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

gggtgcggtc agctgcgagg gcaccggggc ctgcgcctcg cctccggccc 50
ctgcgcctcg accgcgtaga ccgaccccc cctccagcgc gccacccgg 100
tagaggaccc ccgcctgtgc ccgacccgtt ccccgcttt ttgtaaaact 150
taaagcgggc gcagcattaa cgttccccc ccgggtgacc tctcaggggt 200
ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250
ggtcctgagc ctgcagccgc agcagagct caaattccga ggtcccttca 300
ccgatgttgt caccaccaac ctaaagcttg gcaaccgac agaccgaaat 350
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400
caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500
gttcagtcct tgtttgctcc aactgacact tcagatatgg aagcagtatg 550
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650
attatatcca caactgcctc aaagacagaa acaccaatag tgtctaagtc 700
ctcagattct tctttggatg acaccgaagt taagaagggt atggaagaat 750
gtaagaggct gcaagggtgaa gttcagaggc tacgggagga gaacaagcag 800
ttcaagggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900
ggctcttggc tctggtggtt ttgttcttta tcttggtgt aattattggg 950
aagattgctt tctagaggta gcctgcacag gatggtaa at tggattggtg 1000
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttacccctcc 1100
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150
ttagaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200
ctttattaat gacaaggga accatgagta atgccacaat ggcatattgt 1250
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300
tctcttaaaa tgacaccctt cctcgctgtg tgggtgctggc ccttggggag 1350
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catgttttct tattgtcaca agagtacagt taatgctgag tgctgctgaa 1750
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gggagggaaa ttctcagtag tgacagtcac ctctaggcta ccttttttaa 1950
tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
ggacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100
gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200
atgccataaa agaccaacco agttctgttt gactatgtag catcttgaaa 2250
agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

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Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu	20	25	30
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile	50	55	60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val	80	85	90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val	95	100	105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg	110	115	120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val	125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu	155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val	170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala	200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu	215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys	230	235	240

Ile Ala Leu

<210> 285
 <211> 418
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

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ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
cagcagtttt ggggtggggag caagggngga gagaaaactct tcagcgaatc 200
cttctagtag tagttgagag tttgactgtg aattaatttt atgccataaa 250
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aaatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

tattgtaaag gccattttaa accattggta ggccttggtg catgatgctg 50
gattacctcc ttaaattgaca ccttctctcg cctgttggtg ctggcctttg 100
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgaagag 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350
gttcaactta agggaaccaag ctaaattgta ttggttcatg tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450
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gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA
<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

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cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggatttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288

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gcatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200
aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
ntgttggttg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289

<211> 320

<212> DNA

<213> Homo sapiens

<400> 289

tgttttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
tactcgtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgtttg 150
gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
atttaactta tttaatgtat ttcattcat gttttcttat tgtcacaaga 300
gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaaacotttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
gaaacontgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100
ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150
cttctctgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200
ggggagtgcg gtctgctcca cacagtagtc ccangtggc ccantcccg 250
cccaggetgc ttccgtgtc ttcagttctg tccaagccat cagctccttg 300
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400
gcttttgaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
atgcataatt aanttattta atgtatttca tntcatgttt tcttattgtc 550
acaagggtac agttaatgct gcgtgctgct gaantctgtt gggagaantg 600
gtattgctg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

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 cacagtagtc cccacgtggc ccactcccgg cccaggctgc tttccgtgtc 100
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
 gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
 tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300
 tgaagtcaaa ctgttattca gagatgttta atgcataatt aacttattta 350
 atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
 gcgtgctgct gaactctgtt ggggtgaactg gtattgctgc tggagggctg 450
 tgggctcctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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ggctggctga gaggtccca gctgcagcgt ccccgccgc ctctcgga 100
gctctgatct cagctgacag tgcctcggg gaccaaaca gcctggcagg 150
gtctcacttt gttgccagg ctggagttca gtgccatgat catggtttac 200
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250
acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300
atttttcacc cctgggtgga cctcattga tggatctgaa atggaatggg 350
attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400
ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450
tacagtgtgt ggcatcgaat gccagaaaaga actcccaact cccagccttt 500
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aaatatcacc acaaaggag tatctgttag gagaaagaga cagggtgatg 650
gcaccgacag cagggtcagc atcttggaac aaaggttctt aaccaatttc 700
cctttcagca cagctgtgaa gctttccag ggctgtagtg gcattctcat 750
ttccctcag catgttctaa ctgctgccca ctgtgttcat gatggaaagg 800
actatgtcaa agggagtaaa aagctaagg tagggttgtt gaagatgagg 850
aataaaagtg gaggaagaa acgtcgaggt tctaagagga gcaggagaga 900
agctagtggg ggtgaccaa gagaggtac cagagagcat ctgcaggaga 950
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tcgaagggc tgggcacgag gaggcattgg ggacgctacc ttggaactatg 1100
actatgctct tctggagctg aagcgtgctc aaaaaagaa atacatggaa 1150
cttgaatca gcccaacgat caagaaaatg cctgggtggaa tgatccactt 1200
ctcaggattt gataacgata gggctgatca gttggtctat cggttttgca 1250
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aaagaattgg aagcgcaaaa tcattgcggt ctactcaggg caccagtggg 1400

tggatgtcca cggggttcag aaggactaca acgttgetgt tgcacact 1450
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 tcacagagaa aaccagctct gcttaacgta gtgagatcac ttcatagggt 1600
 atgcctggac ttgaactctg tcaatagcat ttcaacattt ttcaaaatca 1650
 ggagattttc gtccatttaa aaaatgtata ggtgcagata ttgaaactag 1700
 gtgggcactt caatgccaa g tatatactct tctttacatg gtgatgagtt 1750
 tcatgttag aaaaattttg ttgccttctt aaaaattaga cacactttaa 1800
 accttcaaac aggtattata aataacatgt gactccttaa tggacttatt 1850
 ctcagggtcc tactctaaga agaataat aggatgctgg ttgtgtatta 1900
 aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
 atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000
 ttcagctcat gccctcaatg tttatattgt gttatctggt gggctctggga 2050
 catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100
 attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150
 caatgtgtat tatttaaaaa tgggagaaat agtttggtct atgaaataaa 2200
 cctagtttag aaataggga gctgagacat tttaagatct caagttttta 2250
 tttaactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300
 cttcacaat tatgaatgat catgtgttga aagccacatt attttatgt 2350
 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400
 tctttttcaa gaaagagtct tttctcctt gacaaaatcc agcttttgta 2450
 tgaggactat agggagaatt ctctgattag taattttaga tatgtccttt 2500
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296
 <211> 413
 <212> PRT
 <213> Homo sapiens

<400> 296
 Met Glu Asn Met Leu Leu Trp Leu Ile Phe Phe Thr Pro Gly Trp
 1 5 10 15
 Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

20	25	30
Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu 35	40	45
Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr 50	55	60
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu 65	70	75
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn 80	85	90
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu 95	100	105
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg 110	115	120
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp 125	130	135
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu 140	145	150
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu 155	160	165
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly 170	175	180
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser 185	190	195
Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala 200	205	210
Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu 215	220	225
Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln 230	235	240
Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys 245	250	255
Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp 260	265	270
Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala 275	280	285
His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys 290	295	300
Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp		

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu		
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser		
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys		
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp		
365	370	375
Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg		
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly		
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 297
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 297
 gcatctgcag gagagagcga aggg 24

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 298
 catcggtccc gtgaatccag aggc 24

<210> 299
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 299
 gaaggagggc cttcctttca gtggaccgg gtcaagaata cccac 45

<210> 300

<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300

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ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tectgagttc 200
caggaccgca cgetccgagg aggaccggga cggcctatgg gatgcctggg 250
gcccatggag tgaatgctca cgcacctggg ggggaggggc ctctactct 300
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450
gaatggcttc ctgtgtctaa tgacctgac aacctatgtt cactcaagtg 500
ccaagccaaa ggaacaaccc tggttgttja actagcacct aaggtcttag 550
atggtacgcg ttgctataca gaatctttgg atatgtgcat cagtggttta 600
tgccaaattg ttggctgcga tcaccagctg ggaagcaccg tcaaggaaga 650
taactgtggg gtctgcaacg gagatgggtc cacttgccgg ctgggtccgag 700
ggcagtataa atcccagctc tccgcaacca aatcggatga tactgtgggt 750
gcaattccct atggaagtag acatattcgc cttgtcttaa aaggtectga 800
tcacttatat ctggaaacca aaacctcca ggggactaaa ggtgaaaaca 850
gtctcagctc cacaggaact ttcttgtgg acaattctag tgtggacttc 900
cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950
agatttcatt gtcaagattc gtaactcggg ctccgtgac agtacagtec 1000
agttcatctt ctatcaaccc atcatccacc gatggaggga gacggatttc 1050
tttcttgcct cagcaacctg tggaggaggt tatcagctga catcggtga 1100
gtgctacgat ctgaggagca accgtgtggt tgctgaccaa tactgtcact 1150
attaccaga gaacatcaaa cccaaaccca agcttcagga gtgcaacttg 1200
gatccttgct cagccagtga cggatacaag cagatcatgc cttatgacct 1250
ctaccatccc ctctctcggg gggaggccac cccatggacc gcgtgctcct 1300

cctcgtgtgg ggggggcac cagagccggg cagtttcttg tgtggaggag 1350
 gacatccagg ggcattgcac ttcagtggaa gagtggaaat gcatgtacac 1400
 ccctaagatg cccatgcgc agccctgcaa cttttttgac tgcctaaaat 1450
 ggctggcaca ggagtggctt ccgtgcacag tgacatgtgg ccagggcctc 1500
 agataccgtg tggctctctg catcgaccat cgaggaatgc acacaggagg 1550
 ctgtagccca aaaacaaagc cccacataaa agaggaatgc atcgtacca 1600
 ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagttgcc 1650
 tggttcaaac aagctcaaga gctagaagaa ggagctgctg tgtcagagga 1700
 gccctcgtaa gttgtaaaag cacagactgt tctatatttg aaactgtttt 1750
 gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800
 taagtgaat catctacca aagctttttg gctctcaaat taaagattga 1850
 ttagtttcaa aaaaaaaaaa 1869

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
1				5					10					15
Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
			80						85					90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
 cggacgcgtg ggcggcggtt gcggaactcc cgtggagggg ccggtgggcc 50
 ctccggccctg acagatggca gtggccactg cggcggcagt actggccgct 100
 ctgggcgggg cgtgtggctt ggcggccccc cggttcgttg ggcccagggt 150
 ccagcgggtg cgcagaggcg gggaccccgg cctcatgcac gggaagactg 200
 tctgtatcac cggggcgaaac agcggccttg gcgcggccac ggcgcgcgag 250
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgcgggg accgcgcgcg 300
 cgcgcgaggag gcggcgggtc agctccgcgc cgagctccgc caggccgcgcg 350
 agtgcggccc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400
 gagctggacc tcgcctcgtt gcgctcggtg cgcgccttct gccaggaaat 450
 gctccaggaa gagcctaggc tggatgtctt gataaataac gcagggatct 500
 tccagtgcgc ttacatgaag actgaagatg ggtttgagat gcagttcggg 550
 gtgaaccatc tggggcaatt tctactcacc aatcttctcc ttggactcct 600
 caaaagtcca gctcccgaca ggattgttgt agttttcttc aaactttata 650
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700
 aaaagctttt gttatagcgc gagcaaactg gctaacattc tttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800
 atcctgggtat tgtacggaca aatctgggga ggcacataca cattccactg 850
 ttggtcaaac cactcttcaa ttggtgtca tgggcttttt tcaaaactcc 900
 agtagaaggt gccagactt ccattttattt ggctcttca cctgaggtag 950
 aaggagtgtc aggaagatac ttgggggatt gtaaagagga agaactgttg 1000
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050
 agtgatgggt ggctgtctaa aataggaaca aggagtaaaa gagctgttta 1100
 taaaactgca tatcagttat atctgtgac aggaatgggtg tggattgaga 1150
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
 ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
 tggatgacat attaataattt gtcagaatta agtgactcaa agtgctatcg 1400
 agagggtttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
 ttactacaat gtttggtgtt tgtgtggaaa ttatctgctt ggtgtgtgca 1500
 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
1				5				10					15	

Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20					25						30

Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
				35				40						45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
				50				55						60

Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
				65				70						75

Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
				80				85						90

Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	95	100	105
Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg	110	115	120
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg	125	130	135
Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr	140	145	150
Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His	155	160	165
Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys	170	175	180
Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr	185	190	195
Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser	200	205	210
Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile	215	220	225
Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val	230	235	240
Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly	245	250	255
Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu	260	265	270
Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr	275	280	285
Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly	290	295	300
Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala	305	310	315
Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val	320	325	330
Met Val Gly Leu Leu Lys	335		

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

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gcaagaaaat tntgggatat cagtgaagtg atgggtngcc tgctaaaata 100
ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250
actgaaaaat tatttttggg ataagagaat ttcagcaaag atgtttttaa 300
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
tggaattat ctgctgggt t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccaggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccattgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cggagcccag ccccttctca acccaaccca acctagccca gtcccagccg 100
ccagcgccctg tccctgtcac ggaccccagc gttaccatgc atcctgcctg 150
cttccctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 200
cgggtttttac tctgttaaca aotgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaacaaa tgcctgatgtt gcttttagtaa atttttatgc 300
tgactgggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450
caaataccca acctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaaattogg gaattagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tajagttttt gaacgagtag cgaatatttt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataacttaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850
gataaatgtg ttctcttgtt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa cttttttacat gccgattgtg acaaatttag 1050
acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
ctattgacag ctttaggcct atgtatgtgt ttggagactt caaagatgta 1150
ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300
 aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
 gctttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
 cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
 tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
 <211> 406
 <212> PRT
 <213> Homo sapiens

<400> 309
 Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser
 1 5 10 15
 Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu
 20 25 30
 Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn
 35 40 45
 Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe
 50 55 60
 Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile
 65 70 75
 Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val
 80 85 90
 Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser
 95 100 105
 Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys
 110 115 120
 Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr
 125 130 135
 Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu
 140 145 150
 Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly
 155 160 165
 Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg
 170 175 180
 Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe
 185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 48
 <223> unknown base

<400> 310

attaaggaag aattttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

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<223> unknown base

<400> 311

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ccagcgctg tccctgtcnc ggancccgag gtnaccatgc atcctgccgt 200
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tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
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<223> Synthetic oligonucleotide probe

<400> 312

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<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgcttctcta tctttaccog acctcagatg ctcccttctg ctcttg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

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gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

tacctgaat ccccttgtae tcccagagta cctcatcac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

ccctctcttg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaacct catgaatgca gatattctag 350

catattgtca gaaggaagga tggtgcaaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

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tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

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 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322

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<212> PRT

<213> Homo sapiens

<400> 322

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Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20				25					30	
Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35				40					45	
Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50				55					60	
Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65				70					75	
Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80				85					90	
Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95				100					105	

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323
<211> 477
<212> DNA
<213> Homo sapiens

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tctaataccc tgaatccctt tgtactcca gactacctca tccacgcttt 100
ctttctgtgc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
atatgcccct cttggcatat catatttggg ggtatatgag tagaccagt 200
atgagtggcc caggactcta tgacctaca accatcatga atgcagatat 250
tctagcatat tgcagaagg aaggatgggt caaattagct ttttatcttc 300
tagcatTTTT ttactacct tatggcatga tctatgtttt ggtgagctct 350
tagaacaaca cacagaagaa ttggtccagt taagtgcctg caaaaagcca 400
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
gaatctgac agttacttta aaaaatg 477

<210> 324
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 324
tataaaaaga cggccagtta aatagacctg caattattaa tct 43

<210> 325
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 325
caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggettaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaacca ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

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ggacccaact ggggtcccg ccgtgctgc tgetgacct ggccttggcc 150
ggaggttcgg ggaccgcttc ggctgaagca ttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctaccc ttgcacacct 250
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ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500
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<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20					25					30	
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35					40					45	
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50					55					60	
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65					70					75	
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80					85					90	
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95					100					105	

Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln	110	115	120
Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met	125	130	135
Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe	140	145	150
Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser	155	160	165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe	170	175	180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu	185	190	195
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu	200	205	210
Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly	215	220	225
Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp	230	235	240
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro	260	265	270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu	275	280	285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg	290	295	300
Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys	305	310	315
Val Asn Leu Ala His Ser Glu Ile	320		

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

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actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250
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<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 47
<223> unknown base

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cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150
tgctgaccat ggccttggcc ggaggttcgg ggaccgcttc ggctgaagca 200
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<210> 333
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 333
acaagctgag ctgctgtgac ag 22

<210> 334
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg ccggagggttc ggggaccgct tcggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

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agggcgcacg gcccgcgacc gagcgtgagg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatgggcgg cggctgggga ttcttgtttg 200
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

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Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
			20					25					30	

Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp	35	40	45
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg	50	55	60
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg	65	70	75
Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	305	310	315

Ser Lys Val Leu Pro Phe Phe Glu Arg	Pro Asp Phe Gln Leu Phe
320	325 330
Thr Gly Asn Lys Ile Gln Asp Glu Glu	Asn Lys Met Leu Leu Leu
335	340 345
Glu Ile Leu His Glu Ile Lys Ser Phe	Pro Leu His Phe Asp Glu
350	355 360
Asn Ser Phe Phe Ala Gly Asp Lys Lys	Glu Ala His Lys Leu Lys
365	370 375
Glu Asp Phe Arg Leu His Phe Arg Asn	Ile Ser Arg Ile Met Asp
380	385 390
Cys Val Gly Cys Phe Lys Cys Arg Leu	Trp Gly Lys Leu Gln Thr
395	400 405
Gln Gly Leu Gly Thr Ala Leu Lys Ile	Leu Phe Ser Glu Lys Leu
410	415 420
Ile Ala Asn Met Pro Glu Ser Gly Pro	Ser Tyr Glu Phe His Leu
425	430 435
Thr Arg Gln Glu Ile Val Ser Leu Phe	Asn Ala Phe Gly Arg Ile
440	445 450
Ser Thr Ser Val Lys Glu Leu Glu Asn	Phe Arg Asn Leu Leu Gln
455	460 465

Asn Ile His

<210> 338

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 101, 263, 376, 397, 426

<223> unknown base

<400> 338

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caagatatct ttacaagag acctgggttag aaaagaaatg gggacacaac 250
attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 341
aaaggaggac ttctgactgc 20

<210> 342
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 342
agagattcat ccactgctcc aagtcg 26

<210> 343
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggoggacg cgtgggttgg gagggggcag 50
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100
ggaattctca taactggacag aaaccgatca ggcattggaac tccccctcgt 150
caactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250
gaatttggtat acagtgtctt acaacatggt ggggggtggac agcgatggat 300
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gtaactatct ccccatccc caggcctgtg cccctctctg gtctctgtct 750
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aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
gcctggcaca gtaactcatg cctgtaatcc caacatthttg ggaggccaac 1400
gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe
1				5					10					15
Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro
				20					25					30
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val
				35					40					45
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala
				50					55					60
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg
				65					70					75
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His
				80					85					90
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn
				95					100					105
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly
				110					115					120

Phe Met Val Ser

<210> 347
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22
<223> unknown base

<400> 347
cacagttccc caccatcaact cntcccatte cttccaactt tattttttage 50
ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
ggagagggac agaggccaga ggactttetca tactggacag aaaccgatca 150
ggcatggaac tccccttctg cactcacctg ttcttgcccc tgggtgttct 200
gacaggtctc tgctcccoct ttaacctgga tgaacatcac ccacgcctat 250
tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300
gggggtggac agcgatggat gctggtgggc gcccctggg atgggccttc 350
agggcgaccgg aggggggacg tttatcgctg cctgtaggg gggggcccaca 400
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
ctcctcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
tggatgatgg 509

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 348
agggacagag gccagaggac ttc 23

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 349
caggtgcata ttcacagcag gatg 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
ggaactcccc ttogtcactc acctgttctt gcccctgggtg ttctt 45

<210> 351
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 351
aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctggggtt tgggcagaaa ggaggggtgt tcggagcccg ccttttctga 100
gcttccctggg ccggtctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatctt ggaaagaaac aatgttctag gtcaaaactga gtctacaaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tjgtttttct acgcattgat tccatgtttg ctacacagatg aagtggccat 350
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tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450
gtcgaatacc aggggggagta cgagagcctg tacacgagcc acatctggat 500
cccagcagc tgggtgtcac tcaactgaagg tctgagtgt gatgtcactg 550
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gggtcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccacc cttaccgcac ctgggatgga gatcaccaaa gatggcttcc 700
acctgggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750
gctactgga ggaggagacc tgggtgccag gaacatgtca aaatggtgag 800
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850
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 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550
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 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccacctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
1				5						10				15

Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
				20					25					30

Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser	35	40	45
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	50	55	60
Gly	Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	65	70	75
Ser	Leu	Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	80	85	90
Leu	Thr	Glu	Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	95	100	105
Thr	Val	Pro	Tyr	Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	110	115	120
Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	125	130	135
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	140	145	150
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	155	160	165
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	170	175	180
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	185	190	195
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	200	205	210
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	215	220	225
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	230	235	240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	245	250	255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	260	265	270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	275	280	285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	290	295	300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					305	310	

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748, 827
<223> unknown base

<400> 353
tctgtctgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50
cttttctagc ttcttgcccg gctctagaac aattcaggct tcgctgcgac 100
tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200
ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250
tcattgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
gcattctgc ctgccccca gaacctctct gtactctcaa ccaacatgaa 350
gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450
tggatcccca gcagctggtg ctcaactcact gaaggtcctg agtgtgatgt 500
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
cattgggctc acagacctca gcctggagca tctgaagca tccctttaat 600
agaaactcaa ccataccttac ccgacctggg atggagatca ccaaagatgg 650
cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
ggcgtgggt tgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
aggcttcgct gcgactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ccaggtcggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgetcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
cccacgcgtc cgcccacgcg tccgagggac aagagagaag agagactgaa 50
acagggagaa gaggcaggag aggaaggagt ggggagagca cgaagctgga 100
ggccgacact gagggagggc gggaggagt gaagaaggag agaggggaga 150
agagggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200
tggagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350
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gogttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600
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 ctgcgcacgg agcgggtctg gaacatcaga tcaaccacca gggcttctct 1050
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 tgggtgtccc catggctcgt gagactcccc ttcgaggatt gcaccgcgcc 1600
 gtctaagcc tccccacaag gcgaggggag ttaccoccaa aacaaagcta 1650
 ttaaagggac agaatactta 1670

<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

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1					5				10					15

Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
				20					25					30

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
				35					40					45

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
					50				55					60

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu	65	70	75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser	80	85	90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg	95	100	105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser	110	115	120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu	125	130	135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn	140	145	150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln	155	160	165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly	170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn	185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile	200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu	215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser	230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile	245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg	260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser	275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg	290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro	305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg	320	325	

<210> 359

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
tctgctgagg tgcagctcat tcac 24

<210> 360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
gaggctctgg aagatctgag atgg 24

<210> 361
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 361
gctctttgt caacgttgcc agtacctcta accattcct cagtcgctc 50

<210> 362
<211> 3038
<212> DNA
<213> Homo sapiens

<400> 362
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ccgccagcct ccgccgcga gctcgttcg tgtcccccgc cctcgtcct 100
gcagctaactg ctcagaaaacg ctggggcgcc caccctggca gactaacgaa 150
gcagctccct tcccacccca actgcaggtc taattttgga cgctttgct 200
gcattttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtatto 250
ctgcagtcag caccacgtc gcccccggac gctcgggtgt caggcccttc 300
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atcctgaggt cattcattat gaagtgtacc ggcggggagt ggctcagagt 500

aaccacagtg ctgttcattg ctagagcaat tccagccatg gtggttccca 550
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tgcagagcag cagtacatgc tggagtgggt cgaaatcacg gtggttatgt 1850
tgatgtaatg cctgtggaca aaagaaagac ctacattgct tcttttcaga 1900
atggaatctt ctcagaaagt ttacagaatc ctccaggagg aaaggcattc 1950

agagtgtttg ctgttgtgtg aaactgaata cttggaagag gaccataaag 2000
 actattccaa atgcaatatt tctgaatttt gtataaaact gtaacattac 2050
 tgtacagagt acatcaacta ttttcagccc aaaaagggtgc caaatgcata 2100
 taaatcttga taaacaaagt ctataaaata aaacatggga cattagcttt 2150
 gggaaaagta atgaaaatat aatgggtttta gaaatcctgt gttaaattatt 2200
 gctatatattt cttagcagtt atttctacag ttaattacat agtcatgatt 2250
 gttctacggt tcatatatta tatgggtgctt tgtatatgcc actaataaaa 2300
 tgaatctaaa cattgaatgt gaatggccct cagaaaatca tctagtgcac 2350
 ttaaaaaataa tgcactctaa aactgaaaga aaccttatca cattttcccc 2400
 agttcaatgc tatgccatta ccaactccaa ataattctca ataattttcc 2450
 acttaataac tgtaaagttt ttttctgtta atttaggcac atagaatatt 2500
 aaattctgat attgcacttc ttattttata taaaataatc ctttaatatc 2550
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 aatgtaataa agtcagagtg gtggtatgaa aacattccta gtgatcatgt 2650
 agtaaagtga gggttaagca tggacagcca gagctttcta tgtactgtta 2700
 aaattgaggt cacatatattt cttttgtatc ctggcaaata ctctgcagg 2750
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 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25					30	

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu	
				35					40					45	
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn	
				50					55					60	
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln	
				65					70					75	
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val	
				80					85					90	
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp	
				95					100					105	
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu	
				110					115					120	
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln	
				125					130					135	
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His	
				140					145					150	
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys	
				155					160					165	
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly	
				170					175					180	
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile	
				185					190					195	
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly	
				200					205					210	
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser	
				215					220					225	
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys	
				230					235					240	
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu	
				245					250					255	
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His	
				260					265					270	
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser	
				275					280					285	
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg	
				290					295					300	
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala	
				305					310					315	

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr	320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile	335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg	350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile	365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr	380	385	390
Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro	395	400	405
Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg	410	415	420
Asr. Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr	425	430	435
Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His	440	445	450
Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro	455	460	465
Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile	470	475	480
Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg	485	490	495
Val Phe Ala Val Val	500		

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
aaccactcca gcatgtactg ctgc 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 369
gaggagacaa ggcagagcg cagcgacgg ccacagacag ccctgggcat 50
ccatcgacgg cgcagcggga gccagcagag ccggaaggcg cgcgccgggc 100
agagaaagcc gagcagagct gggtagcgtc tccgggcgcg cgtccgaacg 150
ggccagcgcc ctccccatgt ccctgtctcc acgcgcgcgc cctccggtea 200
gcatgaggct cctggcgggc gcgctgctcc tgctgctgct ggcgctgtac 250
acgcgcgctg tggacgggtc caaatgcaag tgctcccgga agggacccaa 300
gatecgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtao 400
 cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450
 catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500
 aggggtgaaaa acctcagaag ggaaaaactcc aaaccagttg ggagacttgt 550
 gcaaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600
 aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650
 attgttatga agcacttttt accaacggtc agtttttaca ttttatagct 700
 ggggtgcgaaa ggcttcacga tgggagaccc atctctcttg tgctccagac 750
 ttcctcacag gctgcttttt atcaaaaagg ggaaaactca tgcttttctt 800
 ttttaaaaaa tgcttttttg tatttgctca tacgtcacta tacatctgag 850
 ctttataagc gcccgggagg aacaatgagc ttggtggaca catttcattg 900
 cagtgttgcct ccattcttag ctggggaagc ttccgcttag aggtcctggc 950
 gctcggcac agctgcacg ggctctcttg ggcttatggc cggtcacagc 1000
 ctcagtgtga ctccacagtg gccctgtag ccgggcaagc aggagcaggt 1050
 ctctctgcat ctgttctctg aggaactcaa gtttggttgc cagaaaaatg 1100
 tgcctcattc cccctggtt aatttttaca caccctagga aacatttcca 1150
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 tcccaacctg aggatttctg aaaggttccac aggttcaata tttaatgctt 1250
 cagaagcatg tgaggttccc aacactgtca gcaaaaacct taggagaaaa 1300
 cttaaaaata tatgaataca tgcgcaatac acagctacag acacacattc 1350
 tgttgacaag ggaaaacctt caaagcatgt ttcttttccct caccacaaca 1400
 gaacatgcag tactaaagca atatatttgt gattcccat gtaattcttc 1450
 aatgttaaac agtgcagtc tctttcgaaa gctaagatga ccacgcgcgc 1500
 tttctctgt acatataccc ttaagaacgc cccctccaca caetgcccc 1550
 cagtatatgc cgcattgtac tgctgtgtta tatgctatgt acatgtcaga 1600
 aaccattagc attgcatgca ggtttcatat tctttctaag atggaaagta 1650
 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met	Ser	Leu	Leu	Pro	Arg	Arg	Ala	Pro	Pro	Val	Ser	Met	Arg	Leu
1				5					10					15

Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala
				20				25					30

Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35				40						45

Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50				55						60

Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65				70						75

Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80				85						90

Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
				95				100						105

Arg	Arg	Val	Tyr	Glu	Glu
				110	

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttgagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373
ctccggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374
<211> 3113
<212> DNA
<213> Homo sapiens

<400> 374
gccccaggga ctgctatggc ttcctttggt gttcaccccg gtctgcgtca 50
tgttaaactc caatgtcctc ctgtgggttaa ctgctcttgc catcaagttc 100
accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150
caaaatccgg ggccctaagaa caccgttacc caatgagatc ttgggtccag 200
tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250
cggtttcagc cccagaacc ccgctcctcc tggactggca tccgaaatac 300
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tgcatgacat gctgcccac tggtttaccg ccaatttgga tactttgatg 400
acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450
gcccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500
gtaatgaccg tggatgaagc gaagatattc atgacagaa cagtaagaag 550
cccgtcatgg tctatatcca tgggggatct tacatggagg gcaccggcaa 600
catgattgac ggcagcattt tggcaagcta cggaaacgtc atcgtgatca 650
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tctttggctc gggggctggg gcctcctgtg tcagcctgtt gaccctgtcc 850
cactactcag aaggtctctt ccagaaggcc atcattcaga gcggcacccg 900
cctgtccagc tgggcagtga actaccagcc ggccaagtac actcggatat 950
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cgggagacta tcaagttcat gtacacagac tgggcgata aggaaaaccc 1350
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aaccacaaa cggccagcaa tcaactctgc caacaatccc aaacactcta 2000
aggacctca caaacaggg cctgaggaca caactgtct cattgaaaac 2050
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 aagatcaact tctgacctg tgaaatgtga gaagtacaca tttctgttaa 2750
 aataactgct ttaagatctc taccactcca atcaatgttt agtgtgatag 2800
 gacatcacca tttcaaggcc ccgggtgttt ccaacgtcat ggaagcagct 2850
 gacacttctg aaactcagcc aaggacactt gatatttttt aattacaatg 2900
 gaagtttaaa catttctttc tgtgccacac aatggatggc tctccttaag 2950
 tgaagaaaga gtcaatgaga ttttgcccag cacatggagc tgtaatccag 3000
 agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050
 aatctgtacg gttctgtgca aagaggtgtt ttgccagcct gaactatatt 3100
 taagagactt tgt 3113

<210> 375
 <211> 816
 <212> PRT
 <213> Homo sapiens

<400> 375

Met	Leu	Asn	Ser	Asn	Val	Leu	Leu	Trp	Leu	Thr	Ala	Leu	Ala	Ile
1				5					10					15
Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
				20					25					30
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
				35					40					45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
				50					55					60
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150

Ser Asn Asp Arg Gly Glu Asp Glu Asp	Ile His Asp Gln Asn Ser
155	160 165
Lys Lys Pro Val Met Val Tyr Ile His Gly Gly Ser Tyr Met Glu	
170	175 180
Gly Thr Gly Asn Met Ile Asp Gly Ser	Ile Leu Ala Ser Tyr Gly
185	190 195
Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly	
200	205 210
Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu	
215	220 225
Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly	
230	235 240
Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly	
245	250 255
Ala Gly Ala Ser Cys Val Ser Leu Leu Thr Leu Ser His Tyr Ser	
260	265 270
Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu	
275	280 285
Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile	
290	295 300
Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met	
305	310 315
Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln	
320	325 330
Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile	
335	340 345
Asp Gly Asp Val Ile Pro Asp Asp Pro Gln Ile Leu Met Glu Gln	
350	355 360
Gly Glu Phe Leu Asn Tyr Asp Ile Met Leu Gly Val Asn Gln Gly	
365	370 375
Glu Gly Leu Lys Phe Val Asp Gly Ile Val Asp Asn Glu Asp Gly	
380	385 390
Val Thr Pro Asn Asp Phe Asp Phe Ser Val Ser Asn Phe Val Asp	
395	400 405
Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Thr Leu Arg Glu Thr	
410	415 420
Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Lys Glu Asn Pro Glu	
425	430 435

Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	
440		445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	
455		460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	
470		475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	
485		490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	
500		505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	
515		520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	
530		535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	
545		550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	
560		565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	
575		580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	
590		595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	
605		610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	
620		625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn	
635		640	645
Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	
650		655	660
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	
665		670	675
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	
680		685	690
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	
695		700	705
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	
710		715	720

Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
				725					730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
				740					745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
				755					760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
				770					775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
				785					790					795
Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
				800					805					810
His	Ser	Thr	Thr	Arg	Val									
				815										

<210> 376

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 376

ggcaagctac ggaaacgtca tcgtg 25

<210> 377

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 378

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<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

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				20					25				30	

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Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro			
				50					55					60			
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met			
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Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp			
				80					85					90			
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe			
				95					100					105			
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln			
				110					115					120			
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr			
				125					130					135			
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys			
				140					145					150			
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu			
				155					160					165			
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn			
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Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr			
				185					190					195			
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp			
				200					205					210			
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met			
				215					220					225			
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val			
				230					235					240			
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser			
				245					250					255			
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys			
				260					265					270			
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu			
				275					280					285			
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro			
				290					295					300			
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe			
				305					310					315			

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
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Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
335 340 345

Arg Phe Tyr

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<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
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<210> 382
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 382
cactctccag gctgcatgct cagg 24

<210> 383
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 383
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<210> 384
<211> 3150
<212> DNA
<213> Homo sapiens

<400> 384
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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

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Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile
				20					25					30

Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
				35					40					45

Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
				50					55					60

Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
				65					70					75

Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
				80					85					90

Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
				95					100					105

Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
				110					115					120

Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
				125					130					135

Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser
				140					145					150

Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu
				155					160					165

Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
				170					175					180

Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp
				185					190					195

Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
				200					205					210

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225

Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu	320	325	330
Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 387

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 387

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<210> 388

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 388

gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389

<211> 3313

<212> DNA

<213> Homo sapiens

<400> 389

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ggcgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200

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 ctgtaatccc agtactttgg gaggcgcagg cgggtggatc acctgaggtt 3100
 gggagtttga gaccagcctg accaaccatgg agaaaccccg tctatactaa 3150
 aaaaatacaa aattagccgg gcgtgggtgg gcctgtctgt aatcccagct 3200
 acttgggagg ctgagtcagg agaattgctt taacctggga ggtggaggtt 3250
 gcaatgagct gagattgtgc cattgcactc cagcctgggc aacaagagtg 3300
 aaactctatc tca 3313

<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu	1	5	10	15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	

Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr
860 865 870

Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu
875 880 885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp
890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro
905 910 915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tcgcgtctctg tgaaccgcc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctaggggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc ccagatcca ctgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggtccaga atcgtgtacc aggcagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgogg ccaagacgtg 200
 gatgttcttg ctcttctgtg ggggagcctg ggcaggacac tccagggcac 250
 aggaggacaa ggtgctgggg ggtcatgagt gccaacccca ttgcagcct 300
 tggcaggcgg ccttgttcca gggccagcaa ctactctgtg gcggtgtcct 350
 tgtagggtgc aactgggtcc ttacagctgc ccactgtaaa aaaccgaaat 400
 acacagtaag cctgggagac cacagcctac agaataaaga tggcccagag 450
 caagaaatac ctgtgttca gtccatccca caccctgtct acaacagcag 500
 cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550
 aggcattcct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600
 acccagcctg gccagaagtg caccgtctca ggcgtgggca ctgtcaccag 650
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 tccccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750
 atggtctgtg caggcagcag caaaggggct gacaogtgc agggcgattc 800
 tggaggcccc ctggtgtgtg atggtgcact ccagggcac acatcctggg 850
 gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900
 tgccgtacc tggactggat caagaagatc ataggcagca agggctgatt 950
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
1				5					10					15
Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
				35					40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
				50					55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
				65					70					75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	80	85	90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	95	100	105
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	110	115	120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	125	130	135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	140	145	150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	155	160	165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	170	175	180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	185	190	195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	200	205	210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	215	220	225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	230	235	240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	245	250	255
Ile	Gly	Ser	Lys	Gly											260		

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

caagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaataacct gtggttcagt ccataccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

ggcgccgggtg caacggggcgg gctgagcgcc tcttgccgcc cggcctgcgc 50
gccccggccc gccgcgcgc ccacgcccc accccggccc gcgcccccta 100
gcccccgccc gggcccgcc cccgccccgc gccaggtga gcgctccgcc 150
cgccgagagg ccccgcccc gcccgcccc gcccgcccc ggcggggggg 200
ggaacggggc ggattctctg cgggtcaaac caactgctcc cataaaacat 250
tcatactccc ggccgcccc gctgcgagcg ccccgccagt ccgcgcgcgc 300
gcgcgcctcg cctgtgcgc cctgcgcgc ctgcgcaccc ggggcccgag 350
ccagccaga gccgggcgga gggagcgcg ccgagcctcg tcccgccgcc 400
gggcgggggc cgggcgtag cggcgcgccc tggatgcgga cccggccgcg 450
gggagacggg cgcgcgcgc gaaacgactt tcagtcctcg acgcgcctcg 500
cccaacctt acgatgaaga gggcgctccc tggagggagc cggctgctgg 550
catgggtgct gtggtgcag gctggcagg tggcagccc atgccaggt 600
gctgcgtat gctacaatga gcccaagggt acgacaagt gcccccagca 650
gggcctgcag gctgtgcgc tggcatccc tctgcgagc cagcgcatct 700
tctgcacgg caaccgcctc tcgcatgtgc cagctgcag ctccgtgcc 750
tgccgcaacc tcaccatct gtggtgcac tcgaatgtgc tggcccgaa 800
tgatgcggct gcttcaactg gctggcct cctggagcag ctggacctca 850
cgataatgc acagctccg tctgtggacc ctgccacatt ccacggcctg 900

ggccgectac acacgctgca cctggaccgc tgcggcctgc aggagctggg 950
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 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met	Lys	Arg	Ala	Ser	Ala	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val
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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
				20					25					30
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln
				35					40					45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln
				50					55					60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala
				65					70					75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser
				80					85					90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala
				95					100					105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser
				110					115					120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu
				125					130					135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe
				140					145					150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala
				155					160					165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu
				170					175					180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu
				185					190					195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His
				200					205					210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu
				215					220					225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala
				230					235					240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu
				245					250					255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro
				260					265					270

Leu Trp Ala Trp	Leu Gln Lys Phe Arg	Gly Ser Ser Ser Glu Val
275	280	285
Pro Cys Ser Leu	Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys Arg
290	295	300
Leu Ala Ala Asn	Asp Leu Gln Gly Cys	Ala Val Ala Thr Gly Pro
305	310	315
Tyr His Pro Ile	Trp Thr Gly Arg Ala	Thr Asp Glu Glu Pro Leu
320	325	330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser
335	340	345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys
350	355	360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly
365	370	375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser
380	385	390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro
395	400	405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser
410	415	420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly
425	430	435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu
440	445	450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val
455	460	465
Leu Trp Thr Val	Leu Gly Pro Cys	
470		

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgacct gcagtaacct tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgcaaaag ggaggacggc tgggtcctct 50
ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100
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agetgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200
caaaggcaag tccttttttc cttctcctt ttgggcttat ctctggcggg 250
cgcggcggaa cctagaagct attctgtggt ggaggaaaact gagggcagct 300
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gcgactcggg ccagaacgcc tggctgtcgt accagctgct caaggccacg 2000
gagctcggtc tgttcggcgt gtgggcgcac aatggcgagg tgcgcaccgc 2050
caggtgctg agcgagcgcg acgcggccaa gcacaggctg gtggtgctgg 2100
tcaaggacaa tggcgagcct ccgcgctcgg ccaccgccac gctgcacgtg 2150
ctcctggtgg acggttctc ccagccctac ctgcctctcc cggaggcggc 2200
cccgaccag gcccaggccg acttgctcac cgtctacctg gtggtggcgt 2250

tggcctcggt gtcttcgctc ttctctttt cgggtgctct gttcgtggcg 2300
 gtgcggctgt gtaggaggag cagggcggcc tcggtgggtc gctgcttggt 2350
 gcccagagggc ccccttccag ggcattctgt ggacatgagc ggcaccagga 2400
 ccctatccca gagctaccag tatgaggtgt gtctggcagg aggetcaggg 2450
 accaatgagt tcaagttcct gaagccgatt atccccaact tccctcccca 2500
 gtgccctggg aaagaaatac aaggaaattc taccttcccc aataactttg 2550
 ggttcaatat tcagtgacca tagttgactt ttacattcca taggtatttt 2600
 attttggtgc atttccatgc caatgtttat ttcccccaat ttgtgtgtat 2650
 gtaatatgt acggatttac tcttgatttt tctcatgttc tttctccctt 2700
 tgttttaag tgaacattta cctttattcc tggttctt 2738

<210> 405
 <211> 798
 <212> PRT
 <213> Homo sapiens

<400> 405

Met	Glu	Ala	Ser	Gly	Lys	Leu	Ile	Cys	Arg	Gln	Arg	Gln	Val	Leu
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Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu
			20						25					30
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe
			35						40					45
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe
			50						55					60
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His
			65						70					75
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys
			80						85					90
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu
			95						100					105
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala
			110						115					120
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu
			125						130					135
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly
			140						145					150

Thr	Thr	Phe	Pro	Leu	Lys	Asn	Ala	Glu	Asp	Leu	Asp	Val	Gly	Gln	155	160	165
Asn	Asn	Ile	Glu	Asn	Tyr	Ile	Ile	Ser	Pro	Asn	Ser	Tyr	Phe	Arg	170	175	180
Val	Leu	Thr	Arg	Lys	Arg	Ser	Asp	Gly	Arg	Lys	Tyr	Pro	Glu	Leu	185	190	195
Val	Leu	Asp	Lys	Ala	Leu	Asp	Arg	Glu	Glu	Glu	Ala	Glu	Leu	Arg	200	205	210
Leu	Thr	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Ser	Pro	Pro	Arg	Ser	Gly	215	220	225
Thr	Ala	Gln	Val	Tyr	Ile	Glu	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	230	235	240
Pro	Glu	Phe	Glu	Gln	Pro	Phe	Tyr	Arg	Val	Gln	Ile	Ser	Glu	Asp	245	250	255
Ser	Pro	Val	Gly	Phe	Leu	Val	Val	Lys	Val	Ser	Ala	Thr	Asp	Val	260	265	270
Asp	Thr	Gly	Val	Asn	Gly	Glu	Ile	Ser	Tyr	Ser	Leu	Phe	Gln	Ala	275	280	285
Ser	Glu	Glu	Ile	Gly	Lys	Thr	Phe	Lys	Ile	Asn	Pro	Leu	Thr	Gly	290	295	300
Glu	Ile	Glu	Leu	Lys	Lys	Gln	Leu	Asp	Phe	Glu	Lys	Leu	Gln	Ser	305	310	315
Tyr	Glu	Val	Asn	Ile	Glu	Ala	Arg	Asp	Ala	Gly	Thr	Phe	Ser	Gly	320	325	330
Lys	Cys	Thr	Val	Leu	Ile	Gln	Val	Ile	Asp	Val	Asn	Asp	His	Ala	335	340	345
Pro	Glu	Val	Thr	Met	Ser	Ala	Phe	Thr	Ser	Pro	Ile	Pro	Glu	Asn	350	355	360
Ala	Pro	Glu	Thr	Val	Val	Ala	Leu	Phe	Ser	Val	Ser	Asp	Leu	Asp	365	370	375
Ser	Gly	Glu	Asn	Gly	Lys	Ile	Ser	Cys	Ser	Ile	Gln	Glu	Asp	Leu	380	385	390
Pro	Phe	Leu	Leu	Lys	Ser	Ala	Glu	Asn	Phe	Tyr	Thr	Leu	Leu	Thr	395	400	405
Glu	Arg	Pro	Leu	Asp	Arg	Glu	Ser	Arg	Ala	Glu	Tyr	Asn	Ile	Thr	410	415	420
Ile	Thr	Val	Thr	Asp	Leu	Gly	Thr	Pro	Met	Leu	Ile	Thr	Gln	Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
440	445	450	
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
455	460	465	
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
470	475	480	
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
485	490	495	
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
500	505	510	
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
515	520	525	
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
530	535	540	
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
545	550	555	
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
560	565	570	
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
575	580	585	
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
590	595	600	
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
605	610	615	
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
620	625	630	
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
635	640	645	
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
650	655	660	
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
665	670	675	
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
680	685	690	
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
695	700	705	
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
710	715	720	

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgatc ttgacatgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tctctctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

acccacggt ccgcccacgc gtcgcccac gcgtccgcc acgcgtccgc 50
 ggttagcgt gcgcgattg cctctcgcc tgggcaatgg tcccggtgc 100
 cgtcgacga cgcgcccgcg tcctcggtt cctcggtgg tggcaagtat 150
 tgctgtgggt gctgggactt cccgtccgc gcgtggaggt tgcagaggaa 200
 agtggtcgt tatggtcaga ggagcagct gctcaccctc tccaggtggg 250
 ggtgtgtac ctgggtgagg aggagctct gcatgaccgc atgggcccagg 300
 acagggcagc agaagaggcc aatgcggtgc tggggctgga cacccaaggc 350
 gatcacatgg tgatgctgc tgtgattctt ggggaagctg aggacaaagt 400
 gagttcagag cctagcggcg tcacctgtgg tgetggagga gcggaggact 450
 caaggtgcaa cgtccgagag agcctttct ctctggatgg cgtggagca 500
 cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550
 atctgacga gccccgacag aggactccaa taacactgaa agtctgaaat 600
 ccccaaagggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
 actctgaaaa ttttaaata gtcacaggac cttatggatt ttctgaacc 700
 aaacggtagt gactgtactc tagtctgtt ttacaccccg tggtgccgt 750
 tttctgcag tttggccct cactttaact ctctgcccg ggcatttca 800
 gctcttcaact ttttggcact ggatgcctt cagcacagca gcctttctac 850
 caggtttggc accgtagctg ttctaatat tttattattt caaggagcta 900
 aaccaatggc cagatttaac cacaagatc gaacactgga aacactgaaa 950
 atcttcattt ttaatcagac aggtatagaa gccagaaga atgtggtggt 1000
 aactcaagcc gaccaaatag gccctcttcc cagcaactttg ataaaaagt 1050
 tggactggtt gttgtattt tcttattct ttttaattag ttttattatg 1100
 tatgtaacca ttgaactga gattatcgg tggctaattc caggacaaga 1150
 gcaggaacat gtggagtagt gatggtctga aagaagtgg aaagaggaa 1200
 ttcaatcctt cgtttcagaa attagtcta cagtttcata cttttctcc 1250
 agtgacgtgt tgaactgaaa cttcaggcag attaaaagaa tcatttggtg 1300
 aacaactgaa tgtataaaaa aattataaac tgggtgttta actagtattg 1350
 caataagcaa atgcaaaaat attcaatag 1379

<211> 360
<212> PRT
<213> Homo sapiens

<400> 410

Met	Val	Pro	Ala	Ala	Gly	Arg	Arg	Pro	Pro	Arg	Val	Met	Arg	Leu
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Leu	Gly	Trp	Trp	Gln	Val	Leu	Leu	Trp	Val	Leu	Gly	Leu	Pro	Val
				20					25					30
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu
				35					40					45
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly
				50					55					60
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala
				65					70					75
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His
				80					85					90
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val
				95					100					105
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu
				110					115					120
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly
				125					130					135
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu
				140					145					150
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn
				155					160					165
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg
				170					175					180
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met
				185					190					195
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys
				200					205					210
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser
				215					220					225
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu
				230					235					240
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr
				245					250					255
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly

260	265	270
Ala Lys Pro Met	Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu	
275	280	285
Thr Leu Lys Ile	Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys	
290	295	300
Lys Asn Val Val	Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro	
305	310	315
Ser Thr Leu Ile	Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu	
320	325	330
Phe Phe Leu Ile	Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu	
335	340	345
Ser Ile Arg Trp	Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu	
350	355	360

<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

acacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttct cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgac tgtactctag tctgtttta caccocgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

cccggctccg ctcctctgc cccctcggg tcgcgcgcc acgatgctgc 50
agggccctgg ctgcctgctg ctgctcttc tcgcctcgca ctgctgcctg 100
ggctcggcgc ggggctctt cctctttggc cagcccgact tctcctacaa 150
gcgagcaat tgcaagccca tcccgtcaa cctgcagctg tgccacggca 200
tcgaatacca gaacatgcg ctgccaacc tgctgggcca cgagaccatg 250
aaggaggtgc tggagcaggc cggcgcttg atcccgtgg tcatgaagca 300
gtgccacccg gacaccaaga agttcctgtg ctgcctcttc gccccgtct 350
gcctcgatga cctagacgag accatccagc catgccactc gctctgcctg 400
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gcccagcatg cttgagtgc accgtttccc ccaggacaac gacctttgca 500
tccccctgc tagcagcgac cacctcctgc cagccaccga ggaagctcca 550
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atcacctcgg tgaagcgtg gcagaagggg cagagagagt tcaagcgc 900
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taaggccaca ggagtggata gctgttttca cctaaaggaa aagcccacc 1150
gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser

1	5	10	15
His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln	20	25	30
Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val	35	40	45
Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu	50	55	60
Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln	65	70	75
Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp	80	85	90
Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp	95	100	105
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln	110	115	120
Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro	125	130	135
Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp	140	145	150
Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr	155	160	165
Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp	170	175	180
Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala	185	190	195
Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr	200	205	210
Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn	215	220	225
Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys	230	235	240
Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala	245	250	255
Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile	260	265	270
Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg	275	280	285
Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys			

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
 octggctcgc tgctgctgct c 21

<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 octcacaggt gcaactgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 418
 ctcttctctt ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<400> 419
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 ccgagccccc ggccctgtgc gcgcagcggg gccaccgcac ctacgcgcgc 100
 cgttggtgtg tctgtctcgc gatcagcctg ctcaactgct ccaacgccac 150
 gctgtggctc agctttgcac ctgtggtga cgtcattgct gaggacttgg 200
 tctgtccat ggagcagatc aactggctgt cactggtcta cctcgtggta 250
 tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300
 ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350
 tacgcatggt gccctgcatg gttgttggga cccaaaacc atttgcttc 400

ctcatgggtg gccagagcct ctgtgccctt gccagagcc tggatcatctt 450
ctctccagcc aagctggctg ccttgtggtt cccagagcac cagcgagcca 500
eggccaacat gctcgccacc atgtcgaacc ctctgggctg ccttgtggcc 550
aatgtgctgt cccctgtgct ggtcaagaag ggtgaggaca ttccgttaat 600
gctcgggtgc tataccatcc ctgctggcgt cgtctgctg ctgtccacca 650
tctgcctgtg ggagagtgtg cccccaccc cgcctctgc cggggctgcc 700
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gaacaaggcc tatgtcatcc tggctgtgtg ctgggggga atgatcggga 800
tctctgccag cttctcagcc ctctggagc agatcctctg tgcaagcggc 850
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cacctgctcg ctgctcggc tgtttggctt ctcggtgggc cccgtggcca 1100
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gggagcgaat tacaagcgc cacctgaaaa 1830

<210> 420
<211> 560
<212> PRT
<213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg
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Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp
				20					25					30

Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr
				35					40					45

Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp
				50					55					60

Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr
				65					70					75

Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu
				80					85					90

Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu
				95					100					105

Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val
				110					115					120

Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu
				125					130					135

Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu
				140					145					150

Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met
				155					160					165

Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val
				170					175					180

Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met
				185					190					195

Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser
				200					205					210

Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala
				215					220					225

Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys
				230					235					240

Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys
				245					250					255

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala	Leu Leu
260	265	270	
Glu Gln Ile Leu Cys	Ala Ser Gly His	Ser Ser Gly Phe	Ser Gly
275	280	285	
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly	Ala Leu
290	295	300	
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr	Glu Ala
305	310	315	
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val	Pro Phe
320	325	330	
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu	Ala Ala
335	340	345	
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly	Pro Val
350	355	360	
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly	Glu Gly
365	370	375	
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu	Gly Ile
380	385	390	
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg	Ser Glu
395	400	405	
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu	Asp Trp
410	415	420	
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe	Phe Ser
425	430	435	
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg	Leu Gln
440	445	450	
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val	Gly Gly
455	460	465	
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly	Arg Ala
470	475	480	
Gly Val Leu Gly	Pro Ser Thr Ala Thr	Pro Glu Cys Thr	Ala Arg
485	490	495	
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro	His Pro
500	505	510	
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala	Ala Thr
515	520	525	
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val	Gln Ala
530	535	540	

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
545 550 555

Pro Trp Val Ile Thr
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<210> 421
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
agcttctcag cccctcctgga gcag 24

<210> 422
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 422
cgggtcaata aacctggacg cttgg 25

<210> 423
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 423
tatgtggacc ggaccaagca cttcaactgag gccaccaaga ttg 43

<210> 424
<211> 4313
<212> DNA
<213> Homo sapiens

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 aaaaaaaaaa aaa 4313

<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

Met Met Gln Leu Leu Gln Leu Leu Leu Gly Leu Leu Gly Pro Gly

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Gly Tyr Leu Phe Leu Leu Gly Asp Cys Gln Glu Val Thr Thr Leu	20	25	30
Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val	35	40	45
Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg	50	55	60
Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu	65	70	75
Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg	80	85	90
Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu	95	100	105
Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His	110	115	120
Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe	125	130	135
Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu	140	145	150
Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly	155	160	165
Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe	170	175	180
Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu	185	190	195
Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys	290	295	300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn	305	310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro Asn	320	325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp Val	335	340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln Pro	350	355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala Leu	365	370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val His	380	385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg Thr	395	400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp Arg	410	415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp Gln	425	430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln Ile	440	445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg Tyr	455	460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu Ile	470	475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys Val	485	490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val Ala Ile	500	505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn Tyr	515	520	525
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp Ser	530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser Leu	545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val Leu	560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser Thr	575	580	585

Gly His Leu Leu Val Pro Ile Glu Thr Pro Asn Gly Leu Gly Pro
590 595 600

Ala Gly Thr Asp Thr Pro Pro Leu Ala Thr His Ser Ser Arg Pro
605 610 615

Phe Leu Leu Thr Thr Ile Val Ala Arg Asp Ala Asp Ser Gly Ala
620 625 630

Asn Gly Glu Pro Leu Tyr Ser Ile Arg Asn Gly Asn Glu Ala His
635 640 645

Leu Phe Ile Leu Asn Pro His Thr Gly Gln Leu Phe Val Asn Val
650 655 660

Thr Asn Ala Ser Ser Leu Ile Gly Ser Glu Trp Glu Leu Glu Ile
665 670 675

Val Val Glu Asp Gln Gly Ser Pro Pro Leu Gln Thr Arg Ala Leu
680 685 690

Leu Arg Val Met Phe Val Thr Ser Val Asp His Leu Arg Asp Ser
695 700 705

Ala Arg Lys Pro Gly Ala Leu Ser Met Ser Met Leu Thr Val Ile
710 715 720

Cys Leu Ala Val Leu Leu Gly Ile Phe Gly Leu Ile Leu Ala Leu
725 730 735

Phe Met Ser Ile Cys Arg Thr Glu Lys Lys Asp Asn Arg Ala Tyr
740 745 750

Asn Cys Arg Glu Ala Glu Ser Thr Tyr Arg Gln Gln Pro Lys Arg
755 760 765

Pro Gln Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val
770 775 780

Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His
785 790 795

Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro
800 805 810

Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr
815 820 825

Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu
830 835 840

Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln
845 850 855

Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro
860 865 870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu
1175 1180

<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

gtaagcacat gcctccagag gtgc 24

<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacctt cagtattgat gccaaagacag gccagggtcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

cggacgcgtg ggccggacgcg tgggggagag ccgcagtcac ggctgcagca 50

cctggggagaa ggcagaccgt gtgagggggc ctgtggcccc agcgtgctgt 100

ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150

tgagtttcct catcgactcc agcatcatga ttacctcca gatactattt 200

tttggaatttg ggtggctttt cttcatgcgc caattgttta aagactatga 250

gatacgtcag tatgttgtac aggtgatctt ctccgtgacg tttgcatttt 300

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ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430
<211> 455
<212> PRT
<213> Homo sapiens

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Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser
35 40 45
Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe
50 55 60
Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp
65 70 75
Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val
80 85 90
Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu
95 100 105
His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe
110 115 120
Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser
125 130 135
Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val
140 145 150
Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly
155 160 165
Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn
170 175 180
Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln

	185	190	195
Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala
	200	205	210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser
	215	220	225
Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly
	230	235	240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu
	245	250	255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala
	260	265	270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys	Tyr
	275	280	285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys
	290	295	300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys
	305	310	315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr	Leu
	320	325	330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe
	335	340	345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu
	350	355	360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser
	365	370	375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr
	380	385	390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu
	395	400	405
Tyr Arg Thr Ile	Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe	Asn
	410	415	420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu
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Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro	Glu
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Lys Gln Met Ala	Pro		
	455		

<210> 431

<211> 407
<212> DNA
<213> Homo sapiens

<220>
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<222> 78, 81, 113, 157, 224, 297
<223> unknown base

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ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200
gagctcatca tttttgaaat cttnngagta ttgaatagca gctcccgta 250
cttcaactgg aaaatgaacc tgtgtgtaat tctgctgac ctggttttca 300
tgggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350
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tctccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

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tctgctgac ctggttttca tgggtgccttt ttacattggc tattttattg 350
tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400
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cattctc 457

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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

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<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

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<210> 435

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 435

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<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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a 3951

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 <211> 1141
 <212> PRT
 <213> Homo sapiens

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 Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu
 35 40 45
 Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg
 50 55 60
 Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro
 65 70 75
 Sln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly
 80 85 90
 Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg
 95 100 105

Val Asp Ile Asp	Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu
110	115	120
Asn Gln Trp Leu	Gly Val Ser Val Arg Ser	Gln Gly Pro Gly Gly
125	130	135
Lys Ile Val Thr	Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg Val
140	145	150
Asp Gln Ile Leu	Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe Val
155	160	165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly Glu
170	175	180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln	Gly His Glu Gln Phe Gly
185	190	195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser His
200	205	210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly Thr
215	220	225
Ala Arg Val Glu	Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala His
230	235	240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln Asp
245	250	255
Pro Arg Leu Ile	Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe Ser
260	265	270
Ile Asp Ser Gly	Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser Phe
275	280	285
Val Ala Gly Ala	Pro Arg Ala Asn His	Lys Gly Ala Val Val Ile
290	295	300
Leu Arg Lys Asp	Ser Ala Ser Arg Leu	Val Pro Glu Val Met Leu
305	310	315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala Val
320	325	330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly Ala
335	340	345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val Tyr
350	355	360
Val Tyr Leu Asn	Gln Gly Gly His Trp	Ala Gly Ile Ser Pro Leu
365	370	375
Arg Leu Cys Gly	Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu Ala
380	385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly	Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys	Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro	Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly	Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro	Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg	Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro	Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser	Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro	Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala	Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe	Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr	Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met	Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val	Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln	Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala	His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln	Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val	His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro	Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile	Gly
680	685	690	
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln	Pro
695	700	705	
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val	Met
710	715	720	
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp	Pro
725	730	735	
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His	Val
740	745	750	
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val	Thr
755	760	765	
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr	Thr
770	775	780	
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln	Glu
785	790	795	
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu	Pro
800	805	810	
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe	Ser
815	820	825	
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp	Val
830	835	840	
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly	Gln
845	850	855	
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp	Pro
860	865	870	
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln	Val
875	880	885	
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys	Ser
890	895	900	
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp	Arg
905	910	915	
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly	Glu
920	925	930	
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala	Glu
935	940	945	
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala	Asn
950	955	960	

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

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<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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<210> 442

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

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				20				25					30	

Gly	Arg	Ser	Asp	Gly	Gly	Asn	Phe	Leu	Asp	Asp	Lys	Gln	Trp	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35										40					45				
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				50					55					60					
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
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Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
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Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
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Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305					310					315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					

320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro	Leu Cys Asp Glu Asp Gly	
335	340	345
Tyr Tyr Lys Pro Thr Gln Cys His Gly	Ser Val Gly Gln Cys Trp	
350	355	360
Cys Val Asp Arg Tyr Gly Asn Glu Val	Met Gly Ser Arg Ile Asn	
365	370	375
Gly Val Ala Asp Cys Ala Ile Asp Phe	Glu Ile Ser Gly Asp Phe	
380	385	390
Ala Ser Gly Asp Phe His Glu Trp Thr	Asp Asp Glu Asp Asp Glu	
395	400	405
Asp Asp Ile Met Asn Asp Glu Asp Glu	Ile Glu Asp Asp Asp Glu	
410	415	420
Asp Glu Gly Asp Asp Asp Asp Gly Gly	Asp Asp His Asp Val Tyr	
425	430	435

Ile

<210> 443
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 443
 caaqaatatt cagaagggc aaggg 25

<210> 444
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 444
 catcatgggc atcaccacca tcatcacc 28

<210> 445
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtggtggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

cajactccag atttccctgt caaccacgag gagtccagag aggaaacgcg 50
gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100
cajggatggg cgacaagatc tggctgccct tcccogtget ccttctggcc 150
gctctgcctc cgggtgtgct gcctggggcg gccggcttca caccttccct 200
cgatagcgac ttcaccttta ccttccccgc cggccagaag gagtgcttct 250
accagcccat gccctgaag gcctcgctgg agatcgagta ccaagtttta 300
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350
aaccttagtt tttgaacaaa gaaaatcaga tggagtccac actgtagaga 400
ctgaagttgg tgattacatg ttctgctttg acaatacatt cagcaccatt 450
cttgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500
ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550
tggtatatgaa actggaagac atcttggaat ccatcaacag catcaagtcc 600
agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650
tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700
ctatgggttaa tttagtggtc atggtgggtg tgtcagccat tcaagtttat 750
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaaactc 800
caaaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850
tggtacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900
aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950
tgtgcaagta atcctgctga tccagtgtga cttaagtgtg taacaggaat 1000
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tttctaact ttgaaaaatt ttgcaaatgt cttaggtgat ttaaataaat 1100
gagtattggg cctaattgca acaccagtct gtttttaaca ggttctatta 1150
cccagaactt ttttgtaa at gcggcagtta caaattaact gtggaagttt 1200
tcagttttta gttataaatc acctgagaat tacctaataa tggattgaat 1250

aaatcttttag actacaaaag cccaactttt ctctatttac atatgcatct 1300
ctcctataat gtaaatagaa taatagcttt gaaatacaat taggtttttg 1350
agatttttat aaccaaatac atttcagtgt aacatattag cagaaagcat 1400
tagtctttgt actttgctta cattcccaaa agctgacatt ttcacgattc 1450
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taaataaata tctccttttc tgagctctaa gaattatcag aaaacaggaa 1800
agaatttaga aaaacttgag aaaacctaatt ccaaaaataaa attcaacttaa 1850
gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900
tactcataac ataaatcaaa' ggagatgatt aatttccagt tagctggaag 1950
aaactttggc tgtaggtttt tattttctac aagaattctg gtttgaatta 2000
tttttgtaag caggtacatt ttataaaaatg taagccctac tgtaaggttt 2050
agcactgggt gtacatattt attaaaaatt tttattataa caacttttat 2100
taaaatggcc tttctgaaca ctttatttat tgatgttgaa gtaaggatta 2150
gaaacataga ctccaagtt ttaaacacct aaatgtgaat aacctatata 2200
tacaacaaag tttctgccat ctagcttttt gaagtctatg ggggtcttac 2250
tcaagtacta gtaatttaac ttcacatga atgaactata atttttaagt 2300
tatgcccat tataacgttg ttcattgacta cattgtgagt tagaaacaaa 2350
cttaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400
cttgatgagc aataatgata accagagagt gatttcattt aactcatag 2450
tagtataaaa agagatacat ttccctctta ggccctggg agaagagcag 2500
cttagatttc cctactggca aggtttttta aaatgaggta aatgccgtat 2550
atgatcaatt accttaattg gccaagaaaa tgcttcaggt gtctaggggt 2600
atcctctgca acacttgacg aacaaaggtc aataagatcc ttgcctatga 2650

ataccctcc cttttgcgct gttaaatttg caatgagaag caaattttaca 2700
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 cataacccaa aaagcaaaac ttgtaaacag agtaaaaatc tttaatattt 3050
 ctaaagacat actgtttatc tgcctcatat gcttttttta atttcactat 3100
 tccatttcta aattaaagt atgctaaaatt gagtaagctg tttatcactt 3150
 aacagctcat tttgtctttt tcaatatata aatttttaaaa atactacaat 3200
 atttaactaa ggcccaaccg atttcataa tgtagcagtt accgtgttca 3250
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 aaaaaatgag cacttacaat tgtatgtctc ctcaaagaa gattctttat 3450
 gtgaaatttt aaaagacatt gattccgcat gtaaggattt ttcattctgaa 3500
 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550
 agccattctta aataagcaac gtattgtgag tactgatatg tatataataa 3600
 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
1				5					10					15
Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30
Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45
Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val	Leu Asp Gly Ala Gly	Leu Asp Ile Asp Phe His
	65	70 75
Leu Ala Ser Pro	Glu Gly Lys Thr Leu Val	Phe Glu Gln Arg Lys
	80	85 90
Ser Asp Gly Val	His Thr Val Glu Thr	Glu Val Gly Asp Tyr Met
	95	100 105
Phe Cys Phe Asp	Asn Thr Phe Ser Thr	Ile Ser Glu Lys Val Ile
	110	115 120
Phe Phe Glu Leu	Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln Glu
	125	130 135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu Asp
	140	145 150
Met Lys Leu Glu	Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys Ser
	155	160 165
Arg Leu Ser Lys	Ser Gly His Ile Gln	Ile Leu Leu Arg Ala Phe
	170	175 180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg Val
	185	190 195
Asn Phe Trp Ser	Met Val Asn Leu Val	Val Met Val Val Val Ser
	200	205 210
Ala Ile Gln Val	Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys Arg
	215	220 225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50
agcataccag atctcaccag agagtgcag acaatatgct gcctcccatg 100
gccttgccca gtgtgtcctg gatgetgctt tcttgctca ttctcctgtg 150
ccagggtcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200
gtgtgcctaa aggtcccaag gcctatggct cccctgcta tgccttggtt 250
ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350
cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400
ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450
gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500
ccatcttaaa ccttggccac tgtgggagcc tgtcaagaag cacaggattt 550
ctgaagtgga aagattataa ctgtgatgca aagttacct atgtctgcaa 600
gttcaaggac tagggcaggt gggaaagtcag cagcctcagc ttggcgtgca 650
gtcctcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700
ttctcccaa actgccctac ctgactacct tgctatgata ctcttcttt 750
ttcttttttc ttaccttca ttccaggett ttctctgtct tccatgtctt 800
gagatctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850
aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT

<213> Homo sapiens

<400> 452

Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu
1 5 10 15

Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln
20 25 30

Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
35 40 45

Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser
50 55 60

Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys
65 70 75

Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser
80 85 90

Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly
95 100 105

Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp
110 115 120

Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys
125 130 135

Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser
140 145 150

Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala
155 160 165

Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp
170 175

<210> 453

<211> 550

<212> DNA

<213> Homo sapiens

<400> 453

ccagtcctgtc gccacctcac ttggtgtctg ctgtccccgc caggcaagcc 50

tgggggtgaga gcacagagga gtgggccggg accatgcggg ggacgcggct 100

ggcgctcctg gcgctgtgtc ttggtgcctg cggagagctg gcgcgggcc 150

tgcgctgcta cgtctgtccg gagccacag gagtgtcgga ctgtgtcacc 200

atcgccacct gcaccaccaa cgaaacctg tgcaagacca cactctactc 250

ccgggagata gtgtaccct tccaggggga ctccacgggtg accaagtct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgccgcg 400
tctgaacagc ctccactgcg gggccctcac gtcctccca ctcttgagcc 450
tccgactgta gagtccccgc ccacccccat ggccttatgc ggcccagccc 500
cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaaa aaaaaaaaaa 550

<210> 454
<211> 125
<212> PRT
<213> Homo sapiens

<400> 454
Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala
1 5 10 15
Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu
20 25 30
Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
35 40 45
Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
50 55 60
Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
65 70 75
Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
80 85 90
Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
95 100 105
Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
110 115 120
Leu Ser Leu Arg Leu
125

<210> 455
<211> 1518
<212> DNA
<213> Homo sapiens

<400> 455
ctgcagtcag gactctggga ccgcaggggg ctcccggacc ctgactctgc 50
agccgaaccg gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100
atcttctctt tctttctccc tcttgagtc tcttgagatg atggctctgg 150
gcgcagcggg agctaccgg gtctttgtcg cgatggtagc ggccgctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250
 ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300
 acccaggctc tgcagtcagc gccgcgcggg gaatcctgta cccgggcggg 350
 aataagtacc agaccattga caactaccag ccgtaccgt gcgcagagga 400
 cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450
 acgcaggcgt gcaaactctgt ctgcctgca ggaagcgccg aaaacgctgc 500
 atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550
 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600
 ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650
 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700
 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750
 tctggtccaa gatctgtaaa cctgtcctga aagaaggcca agtgtgtacc 800
 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850
 ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900
 gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950
 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050
 gcattccaat aacaccttcc aaaaacctgg agtgtaagag ctttgtttct 1100
 ttatggaact cccctgtgat tgcagtaaat tactgtattg taaattctca 1150
 gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200
 ggtgctgcac tgccatttt tccctctgtt atgtaaattt ttgtacacat 1250
 tgattgttat cttgactgac aaatattcta tattgaaactg aagtaaatca 1300
 tttcagctta tagttcttaa aagcataacc ctttacccca ttttaattcta 1350
 gagtctagaa cgcaaggatc tcttggaatg acaaatgata ggtacctaaa 1400
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450
 ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500
 catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

Met	Met	Ala	Leu	Gly	Ala	Ala	Gly	Ala	Thr	Arg	Val	Phe	Val	Ala
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Met	Val	Ala	Ala	Ala	Leu	Gly	Gly	His	Pro	Leu	Leu	Gly	Val	Ser
				20					25					30

Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu
				35					40					45

Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val
				50					55					60

Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln
				65					70					75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu
				80					85					90

Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp
				95					100					105

Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg
				110					115					120

Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn
				125					130					135

Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile
				140					145					150

Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu
				155					160					165

Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His
				170					175					180

Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys
				185					190					195

Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys
				200					205					210

Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg
				215					220					225

Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly
				230					235					240

Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser
				245					250					255

Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His				
				260					265					

<210> 457
<211> 638
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,
509, 556
<223> unknown base

<400> 457
tgtgtttccc tgcagtcaga atttgggacn gcaggggttc ccggacctga 50
ttttgcagcg gaacgggaag gttttgtggg acccaggttg aaatgacggg 100
natttttttt tttttctcct tcnngagtc tnttgagang atggtttttg 150
gggcagcggg agctaaccgc gttttttgtg gcgatggtag cggcggtttt 200
cggcgccac cttntgctgg gagtgagcgc cacttgaat cggtttttaa 250
ttccaaacgt atcaagaacc tgccccacc gntggcggc gctgcggggc 300
abccagntt tgcagtcagc gccgcgcgc gaatcctgta ccggggcggg 350
aataagtacc agaccattga caattaccag ccgtaccctg gcgcagagga 400
cgaggagtgc ggcactgat agtaactggc tagtcccacc cggcgagggg 450
angcgggcgt gcaaatntgt ntngcctgca ggaagcgccg aaaacgctgc 500
atgcgtcang ctatgtctg ccccggaat tactgcaaaa atggaatatg 550
tgtgtnttct gatcaaaatc atttcgagg agaaattgag gaaaccatca 600
ctgaaagctt tgtaatgat catagcaact tggatggg 638

<210> 458
<211> 4040
<212> DNA
<213> Homo sapiens

<400> 458
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acctaccaa tccgtgcgc cgcgctggg ccgtcggaga gtgcgtgtgc 100
ttctctcctg cgcgggtgc ttgggctcgg ccaggcgggg tccgcgcga 150
gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200
gtatatTTTT gtggaatgaa aagggaagtat tagaaatgag ctgaagacca 250
ttcacagatt aatatTTTT gggacagatt tgtgatgctt gattcaccct 300

tgaagtaatg tagacagaag ttctcaaatt tgcatattac atcaactgga 350
accagcagtg aatcttaaatg ttcaacttaa tcagaacttg cataagaaag 400
agaatgggag tctgggttaa taaagatgac tatatcagag acttgaaaag 450
gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500
atcaggatgt ttacagttta cttggagtgt ccaaaactgc aagcagtaga 550
gaaataagac aagctttcaa gaaattggca ttgaagttac atcctgataa 600
aaaccogaat aacccaaatg cacatggcga ttttttaaaa ataaatagag 650
catatgaagt actcaaagat gaagatctac ggaaaaagta tgacaaatat 700
ggagaaaaag gacttgagga taatcaaggt ggccagtatg aaagctggaa 750
ctattatcgt tatgattttg gtatttatga tgatgatcct gaaatcataa 800
cattggaaag aagagaattt gatgctgctg ttaattctgg agaactgtgg 850
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<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

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Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val
			20						25				30	

Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40				45	

Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55				60	

Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70				75	

Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	80	85	90
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	95	100	105
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	110	115	120
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	125	130	135
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	140	145	150
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	155	160	165
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	170	175	180
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	185	190	195
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly	200	205	210
Met	Ala	Pro	Val	Lys	Tyr	His	Gly	Asp	Arg	Ser	Lys	Glu	Ser	Leu	215	220	225
Val	Ser	Phe	Ala	Met	Gln	His	Val	Arg	Ser	Thr	Val	Thr	Glu	Leu	230	235	240
Trp	Thr	Gly	Asn	Phe	Val	Asn	Ser	Ile	Gln	Thr	Ala	Phe	Ala	Ala	245	250	255
Gly	Ile	Gly	Trp	Leu	Ile	Thr	Phe	Cys	Ser	Lys	Gly	Gly	Asp	Cys	260	265	270
Leu	Thr	Ser	Gln	Thr	Arg	Leu	Arg	Leu	Ser	Gly	Met	Leu	Phe	Leu	275	280	285
Asn	Ser	Leu	Asp	Ala	Lys	Glu	Ile	Tyr	Leu	Glu	Val	Ile	His	Asn	290	295	300
Leu	Pro	Asp	Phe	Glu	Leu	Leu	Ser	Ala	Asn	Thr	Leu	Glu	Asp	Arg	305	310	315
Leu	Ala	His	His	Arg	Trp	Leu	Leu	Phe	Phe	His	Phe	Gly	Lys	Asn	320	325	330
Glu	Asn	Ser	Asn	Asp	Pro	Glu	Leu	Lys	Lys	Leu	Lys	Thr	Leu	Leu	335	340	345
Lys	Asn	Asp	His	Ile	Gln	Val	Gly	Arg	Phe	Asp	Cys	Ser	Ser	Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln Asn Phe
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Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys Val
665 670 675

Lys Ala Gly Lys Val Asp Cys Gln Ala Tyr Ala Gln Thr Cys Gln
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Glu Arg Ala Lys Arg Asn Phe Gln Glu Glu Gln Ile Asn Thr Arg
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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<210> 462

<211> 50

<212> DNA

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<211> 1818

<212> DNA

<213> Homo sapiens

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<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

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				20					25					30
Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly
				35					40					45
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln
				50					55					60
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu
				65					70					75
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr
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Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn
				95					100					105
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn
				110					115					120
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu
				125					130					135
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp
				140					145					150
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly

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170	175	180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe		
185	190	195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly		
200	205	210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe		
215	220	225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp		
230	235	240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys		
245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln		
260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln		
275	280	285
Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys		
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<211> 1547

<212> DNA

<213> Homo sapiens

<400> 465

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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
			20						25					30

Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
			35						40					45

Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
			50						55					60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser	65	70	75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln	80	85	90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp	95	100	105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln	110	115	120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser	125	130	135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro	140	145	150
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala	155	160	165
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg	170	175	180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro	185	190	195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala	200	205	210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys	215	220	225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys	230	235	240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	245	250	255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	260	265	270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	275	280	285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	290	295	300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	305	310	315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	320	325	330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	335	340	345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg
350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser
365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln
380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr
395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp
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<210> 467

<211> 1071

<212> DNA

<213> Homo sapiens

<400> 467

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<210> 468
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 468

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				20					25					30
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
				110					115					120
Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn
				125					130					135
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln
				140					145					150
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr
				155					160					165
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn
				170					175					180
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu
				185					190					195
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met
				200					205					210

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215				220						225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230				235						240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245				250						255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
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 <211> 687
 <212> DNA
 <213> Homo sapiens

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<210> 470
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 470
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 20 25 30

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Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu
				50					55					60
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn
				65					70					75
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu
				80					85					90
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile
				95					100					105
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg
				110					115					120
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp
				125					130					135
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg
				140					145					150
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln
				155					160					165
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe
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<210> 471

<211> 2368

<212> DNA

<213> Homo sapiens

<400> 471

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<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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				20					25					30
Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser
				35					40					45
Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr
				50					55					60
Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu
				65					70					75
Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys
				80					85					90
Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
				95					100					105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
				110					115					120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
				125					130					135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
				140					145					150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
				155					160					165

Ile Ser Gly Lys	Ile Trp His Leu His	Asn Tyr Phe Thr Val Thr
170	175	180
Leu Gly Ile Pro	Ala Trp Cys Ser Tyr Val	Phe Phe Val Ile Ala
185	190	195
Thr Leu Val Phe	Gly Leu Phe Met Gly	Leu Val Leu Val Val Ile
200	205	210
Ser Glu Cys Phe	Tyr Val Pro Leu Pro	Arg His Leu Ser Glu Arg
215	220	225
Ser Glu Gln Asn	Arg Arg Ser Glu Glu	Ala His Arg Ala Glu Gln
230	235	240
Leu Gln Asp Ala	Glu Glu Glu Lys Asp	Asp Ser Asn Glu Glu Glu
245	250	255
Asn Lys Asp Ser	Leu Val Asp Asp	Glu Glu Lys Glu Asp Leu
260	265	270
Gly Asp Glu Asp	Glu Ala Glu Glu Glu	Glu Glu Glu Asp Asn Leu
275	280	285
Ala Ala Gly Val	Asp Glu Glu Arg Ser	Glu Ala Asn Asp Gln Gly
290	295	300
Pro Pro Gly Glu	Asp Gly Val Thr Arg	Glu Glu Val Glu Pro Glu
305	310	315
Glu Ala Glu Glu	Gly Ile Ser Glu Gln	Pro Cys Pro Ala Asp Thr
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<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

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<210> 474

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

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<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 477
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 35 40 45
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile
 50 55 60
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
 65 70 75
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
 80 85 90
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
 95 100 105
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
 110 115 120
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
 125 130 135
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
 140 145 150
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
 155 160 165
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser
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 Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
 185 190 195
 Glu Lys Lys Phe Ser Met
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<210> 478

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 478
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<210> 479
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 479
acaagtgtct tcccaacctg 20

<210> 480
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 480
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<210> 481
<211> 51
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

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<210> 482
<211> 3819
<212> DNA
<213> Homo sapiens

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<211> 693

<212> PRT

<213> Homo sapiens

<400> 483

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				20					25					30
Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	Asn	Gln	Thr	His	Arg	Ser	Ser
				35					40					45
Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	Arg	Ile	Ser	Ile	Glu	Asn
				50					55					60
Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	Phe	Pro	Ala	Ala	His
				65					70					75
Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe
				80					85					90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

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395	400 405
Leu Ser Tyr Val Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val
410	415 420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg
425	430 435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu
440	445 450
Leu Ala Val Phe Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro
455	460 465
Val Ala Leu Thr Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile
470	475 480
Phe Leu His Phe Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu
485	490 495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr
500	505 510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly
515	520 525
Phe Pro Ile Phe Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp
530	535 540
Asn Tyr Gly Pro Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly
545	550 555
Val Ile Tyr Pro Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser
560	565 570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn
575	580 585
Met Ala Met Leu Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg
590	595 600
Pro His Thr Gln Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu
605	610 615
Ser Leu Val Leu Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe
620	625 630
Ala Ser Gly Thr Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile
635	640 645
Ile Thr Ser Phe Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser
650	655 660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

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<211> 516
<212> DNA
<213> Homo sapiens

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<222> 68, 70, 84, 147
<223> unknown base

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cgggtggccct gacaggtct gaaggctggc tgcgagcca gtgcatctt 200
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<211> 22
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 485
ggcattggag cagtgtggg tg 22

<210> 486
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 486

tggaggccta gatgcggctg gacg 24

<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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				20					25					30			
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln			
				35					40					45			
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser			
				50					55					60			
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp			
				65					70					75			
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe			
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Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys			
				95					100					105			
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu			
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Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser			
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Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe			
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Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro			
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Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala	170	175	180
Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr	185	190	195
Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu	200	205	210
Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys	215	220	225
Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu	230	235	240
Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe	245	250	255
Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe	260	265	270
Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala	275	280	285
Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys	290	295	300
Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr	305	310	315
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu	320	325	330
His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly	335	340	345

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

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<223> Synthetic oligonucleotide probe

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

Met	Val	Phe	Pro	Met	Trp	Thr	Leu	Lys	Arg	Gln	Ile	Leu	Ile	Leu	1	5	10	15
Phe	Asn	Ile	Ile	Leu	Ile	Ser	Lys	Leu	Leu	Gly	Ala	Arg	Trp	Phe	20	25	30	
Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	35	40	45	
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	50	55	60	
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	65	70	75	
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His	80	85	90	
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu	95	100	105	
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro	110	115	120	
Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp	125	130	135	
Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu	140	145	150	
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys	155	160	165	
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	170	175	180	
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	185	190	195	

Glu Lys Asp Ala Phe Leu Asn Leu Thr	Lys Leu Lys Val Leu Ser
200	210
Leu Lys Asp Asn Asn Val Thr Ala Val	Pro Thr Val Leu Pro Ser
215	225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn	Asn Met Ile Ala Lys Ile
230	240
Gln Glu Asp Asp Phe Asn Asn Leu Asn	Gln Leu Gln Ile Leu Asp
245	255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr	Asn Ala Pro Phe Pro Cys
260	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu	Gln Ile Pro Val Asn Ala
275	285
Phe Asp Ala Leu Thr Glu Leu Lys Val	Leu Arg Leu His Ser Asn
290	300
Ser Leu Gln His Val Pro Pro Arg Trp	Phe Lys Asn Ile Asn Lys
305	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn	Phe Leu Ala Lys Glu Ile
320	330
Gly Asp Ala Lys Phe Leu His Phe Leu	Pro Ser Leu Ile Gln Leu
335	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln	Val Tyr Arg Ala Ser Met
350	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu	Lys Ser Leu Lys Ile Leu
365	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu	Leu Lys Ser Phe Asn Leu
380	390
Ser Pro Leu His Asn Leu Gln Asn Leu	Glu Val Leu Asp Leu Gly
395	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu	Ser Met Phe Lys Gln Phe
410	420
Lys Arg Leu Lys Val Ile Asp Leu Ser	Val Asn Lys Ile Ser Pro
425	435
Ser Gly Asp Ser Ser Glu Val Gly Phe	Cys Ser Asn Ala Arg Thr
440	450
Ser Val Glu Ser Tyr Glu Pro Gln Val	Leu Glu Gln Leu His Tyr
455	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser	Cys Arg Phe Lys Asn Lys
470	480

Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	485	490	495
Gln	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	500	505	510
Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	515	520	525
Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	530	535	540
Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	545	550	555
Leu	Leu	His	Ser	Thr	Ala	Phe	Glu	Glu	Leu	His	Lys	Leu	Glu	Val	560	565	570
Leu	Asp	Ile	Ser	Ser	Asn	Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile	575	580	585
Thr	His	Met	Leu	Asn	Phe	Thr	Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys	590	595	600
Leu	Met	Met	Asn	Asp	Asn	Asp	Ile	Ser	Ser	Ser	Thr	Ser	Arg	Thr	605	610	615
Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu	Glu	Phe	Arg	Gly	Asn	His	620	625	630
Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn	Arg	Tyr	Leu	Gln	Leu	635	640	645
Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp	Ile	Ser	Lys	Asn	650	655	660
Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly	Met	Pro	Pro	665	670	675
Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys	Ser	Phe	680	685	690
Ser	Trp	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu	Asp	695	700	705
Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn	710	715	720
Cys	Ser	Arg	Ser	Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	725	730	735
Arg	Ser	Leu	Thr	Lys	Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	740	745	750
Tyr	Leu	Asp	Leu	Ser	Ser	Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr	755	760	765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu
770 775 780

His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val
785 790 795

Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr
800 805 810

Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val
815 820 825

Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu
830 835 840

Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val
845 850 855

Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile
860 865 870

Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile
875 880 885

Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys
890 895 900

Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys
905 910 915

Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu
920 925 930

Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln
935 940 945

Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys
950 955 960

Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His
965 970 975

Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe
980 985 990

Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys
995 1000 1005

Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln
1010 1015 1020

Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr
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Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val
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<211> 4199
<212> DNA
<213> Homo sapiens

<400> 497
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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

Met	Glu	Asn	Met	Phe	Leu	Gln	Ser	Ser	Met	Leu	Thr	Cys	Ile	Phe
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Leu	Leu	Ile	Ser	Gly	Ser	Cys	Glu	Leu	Cys	Ala	Glu	Glu	Asn	Phe
				20					25				30	

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40				45	

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
				50					55				60	

Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70				75	

Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85				90	

Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100				105	

Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115				120	

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130				135	

Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145				150	

Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160				165	

Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175				180	

Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190				195	

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205				210	

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220				225	

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235				240	

Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly	245	250	255
Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys	260	265	270
Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn	275	280	285
Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg	290	295	300
Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val	305	310	315
Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Val Ser Gly	320	325	330
Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser	335	340	345
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser	350	355	360
Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg	365	370	375
Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu	380	385	390
Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe	395	400	405
Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu	410	415	420
Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys	425	430	435
Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His	440	445	450
Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser	455	460	465
Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala	470	475	480
Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe	485	490	495
Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu	500	505	510
Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu	515	520	525

Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr	Asn Asn
530		535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser	Asp
545		550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg	Ile
560		565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr	Asn
575		580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu	Thr
590		595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val	Phe
605		610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn	Arg
620		625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu	Asp
635		640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe	Leu
650		655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn	Met
665		670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg	Leu
680		685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr	Asp
695		700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu	Ser
710		715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu	Val
725		730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys	Thr
740		745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu	Ser
755		760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp	Ile
770		775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys	Ile
785		790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln	Arg
800		805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp
815 820 825

Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr
830 835 840

Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp
845 850 855

Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr
860 865 870

Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser
875 880 885

Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu
890 895 900

Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu
905 910 915

Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp
920 925 930

Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val
935 940 945

Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe
950 955 960

Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile
965 970 975

Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu
980 985 990

Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro
995 1000 1005

Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn
1010 1015 1020

Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val
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Asp Ser Ile Lys Gln Tyr
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<400> 503
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<210> 504
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<211> 1738
<212> DNA
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<210> 506

<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60

Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75

Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90

Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105

Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120

Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135

Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150

Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
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Gly Pro Pro Arg Val Ala Pro Asn Pro	Thr Gly Val Asp Ser Ala	
185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln	Ser Arg Val Asp Leu Leu	
200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala	Pro Leu His Ser Leu Ala	
215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro	Asp Pro Gly Ser Leu Leu	
230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser Glu	
245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys Lys	
260	265	270
Lys Asp Ser		

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 <211> 273
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
 35 40 45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	155	160	165
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	170	175	180
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	185	190	195
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	200	205	210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	215	220	225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	230	235	240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	245	250	255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	260	265	270

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

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<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60

Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75

Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90

Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105

Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120

Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135

Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150

Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
				155					160					165

Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly
				170					175					180

Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala
				185					190					195

Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu
				200					205					210

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225

Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
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Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
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Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

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<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

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<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 513

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<210> 514

<211> 2690

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2039-2065

<223> unknown base

<400> 514

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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

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20										25					30				
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile					
				35					40					45					
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu					
				50					55					60					
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu					
				65					70					75					
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp					
				80					85					90					
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile					
				95					100					105					
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln					
				110					115					120					
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile					
				125					130					135					
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro					
				140					145					150					
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe					
				155					160					165					
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn					
				170					175					180					
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr					
				185					190					195					
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser					
				200					205					210					
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr					
				215					220					225					
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val					
				230					235					240					
Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr					
				245					250					255					
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val					
				260					265					270					
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu					
				275					280					285					
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly					
				290					295					300					
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln					

305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu		
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu		
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala		
350	355	360
Glu Ala Glu Lys		

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 tgaattaggt attataggga tggtaggggtt gatttttntt cctggaggct 100
 tttagctttg gactctcnct ttctcccaca gagcncttcg accatcactg 150
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
 tcttcacctt ttntctctcc cncctcacia tctatgtctt cgccttcaac 250
 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 517
 caacgtgatt tcaaagctgg gctc 24

<210> 518
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gcc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatgggtg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

gttgtgtcct tcagcaaaac agtggattta aatctccttg cacaagcttg 50

agagcaacac aatctatcag gaaagaaaga aagaaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300

gtgcactatt gacaaccggg tcacccgggt ggcttggtta aaccgcagca 350

ccatcctcta tgctgggaat gacaagtggg gcctggatcc tcgctgggtc 400

cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450
 tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500
 caaagacctc taggggccac ctcatgtgc aagtatctcc caaaattgta 550
 gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600
 ctgcatagca actggtagac cagagcctac ggttacttgg agacacatct 650
 ctcccaaagc ggttggtctt gtgagtgaag acgaatactt ggaaattcag 700
 ggcacacccc gggagcagtc aggggactac gagtgcagtg cctccaatga 750
 cgtggccgcg cccgtggtac ggagagtaaa ggtcacctg aactatccac 800
 catacatttc agaagccaag ggtacaggtg tccccgtggg aaaaagggg 850
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 caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300
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 aaaaagaaat tgaaaattgc cttgcagata tttaggtaca atggagtttt 1400
 cttttcccaa acgggaagaa cacagcacac ccggttgga cccactgcaa 1450
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 aattcaatca gtccatagag acgaacagaa tgagaccttc cggccaagc 1600
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 aaacgtgaaa taaaagagc aaaaaaaaa 1679

<210> 523
 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 523

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Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro
			20						25					30
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val
			35						40					45
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp
			50						55					60
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu
			65						70					75
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu
			80						85					90
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val
			95						100					105
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp
			110						115					120
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser
			125						130					135
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly
			140						145					150
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro
			155						160					165
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val
			170						175					180
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln
			185						190					195
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro
			200						205					210
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile
			215						220					225
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr
			230						235					240
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp
			245						250					255
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys
			260						265					270
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val
			275						280					285

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
335 340

<210> 524

<211> 503

<212> DNA

<213> Homo sapiens

<400> 524

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tgggcaatct tcacggggct ggctgctctg tgtctcttcc aaggagtgcc 100
cgtgcgcagc ggagatgcc cctccccaa agctatggac aacgtgacgg 150
tccggcaggg ggagagcgcc accctcaggt gcactattga caaccgggtc 200
accgggtgg cctggctaaa ccgcagcacc atctctatg ctgggaatga 250
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agtacagcat cgagatccag aacgtggatg tgtatgacga gggcccttac 350
acctgctcgg tgcagacaga caaccacca aagacctcta gggccacct 400
cattgtgcaa gtatctcca aaattgtaga gatttcttca gatatctcca 450
ttaatgaagg gaacaatatt agctcacct gcatagcaac tggtagacca 500
gag 503

<210> 525

<211> 2602

<212> DNA

<213> Homo sapiens

<400> 525

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tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150
aaggggacaa gacagctgtt aggctcacgc acgcagctgg agctggtctt 200
agcaggtgcc tctctactgc tggctgcact gcttctgggc tgcttgtgg 250

ccctaggggt ccagtaccac agagacccat cccacagcac ctgcettaca 300
gaggcctgca ttcgagtggc tggaaaaatc ctggagtccc tggaccgagg 350
ggtgagcccc tgtgaggact tttaccagtt ctctgtggg ggctggattc 400
ggaggaaccc cctgcccgat gggcggttctc gctggaacac cttcaacagc 450
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cttcaactcc agcagtgaag ctgagcagaa gacacagcgc ttctacctat 550
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 cc 2602

<210> 526
 <211> 736
 <212> PRT
 <213> Homo sapiens

<400> 526
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 Phe Gln Lys Gly Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu
 20 25 30
 Glu Leu Val Leu Ala Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu
 35 40 45
 Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro
 50 55 60

Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly	
				65					70					75	
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp	
				80					85					90	
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu	
				95					100					105	
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp	
				110					115					120	
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe	
				125					130					135	
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu	
				140					145					150	
Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro	
				155					160					165	
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly	
				170					175					180	
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala	
				185					190					195	
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala	
				200					205					210	
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser	
				215					220					225	
Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala	
				230					235					240	
Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu	
				245					250					255	
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met	
				260					265					270	
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val	
				275					280					285	
Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met	
				290					295					300	
Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu	
				305					310					315	
Glu	Phe	Leu	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Glu	Leu	Ser	Asp	Ser	
				320					325					330	
Glu	Pro	Val	Val	Val	Tyr	Gly	Met	Asp	Tyr	Leu	Gln	Gln	Val	Ser	
				335					340					345	

Glu Leu Ile Asn Arg Thr Glu Pro Ser	Ile Leu Asn Asn Tyr Leu
350	355 360
Ile Trp Asn Leu Val Gln Lys Thr Thr	Ser Ser Leu Asp Arg Arg
365	370 375
Phe Glu Ser Ala Gln Glu Lys Leu Leu	Glu Thr Leu Tyr Gly Thr
380	385 390
Lys Lys Ser Cys Val Pro Arg Trp Gln	Thr Cys Ile Ser Asn Thr
395	400 405
Asp Asp Ala Leu Gly Phe Ala Leu Gly	Ser Leu Phe Val Lys Ala
410	415 420
Thr Phe Asp Arg Gln Ser Lys Glu Ile	Ala Glu Gly Met Ile Ser
425	430 435
Glu Ile Arg Thr Ala Phe Glu Glu Ala	Leu Gly Gln Leu Val Trp
440	445 450
Met Asp Glu Lys Thr Arg Gln Ala Ala	Lys Glu Lys Ala Asp Ala
455	460 465
Ile Tyr Asp Met Ile Gly Phe Pro Asp	Phe Ile Leu Glu Pro Lys
470	475 480
Glu Leu Asp Asp Val Tyr Asp Gly Tyr	Glu Ile Ser Glu Asp Ser
485	490 495
Phe Phe Gln Asn Met Leu Asn Leu Tyr	Asn Phe Ser Ala Lys Val
500	505 510
Met Ala Asp Gln Leu Arg Lys Pro Pro	Ser Arg Asp Gln Trp Ser
515	520 525
Met Thr Pro Gln Thr Val Asn Ala Tyr	Tyr Leu Pro Thr Lys Asn
530	535 540
Glu Ile Val Phe Pro Ala Gly Ile Leu	Gln Ala Pro Phe Tyr Ala
545	550 555
Arg Asn His Pro Lys Ala Leu Asn Phe	Gly Gly Ile Gly Val Val
560	565 570
Met Gly His Glu Leu Thr His Ala Phe	Asp Asp Gln Gly Arg Glu
575	580 585
Tyr Asp Lys Glu Gly Asn Leu Arg Pro	Trp Trp Gln Asn Glu Ser
590	595 600
Leu Ala Ala Phe Arg Asn His Thr Ala	Cys Met Glu Glu Gln Tyr
605	610 615
Asn Gln Tyr Gln Val Asn Gly Glu Arg	Leu Asn Gly Arg Gln Thr
620	625 630

Leu Gly Glu Asn Ile Thr Asp Asn Gly Gly Leu Lys Ala Ala Tyr		
635	640	645
Asn Ala Tyr Lys Ala Trp Leu Arg Lys His Gly Glu Glu Gln Gln		
650	655	660
Leu Pro Ala Val Gly Leu Thr Asn His Gln Leu Phe Phe Val Gly		
665	670	675
Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser Ser His		
680	685	690
Glu Gly Leu Val Thr Asp Pro His Ser Pro Ala Arg Phe Arg Val		
695	700	705
Leu Gly Thr Leu Ser Asn Ser Arg Asp Phe Leu Arg His Phe Gly		
710	715	720
Cys Pro Val Gly Ser Pro Met Asn Pro Gly Gln Leu Cys Glu Val		
725	730	735

Trp

<210> 527
 <211> 4308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 1478, 3978, 4057-4058, 4070
 <223> unknown base

<400> 527
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 ccgctcccgcc ccgcgcgcgc gcgcgcgcgc agagcccccc gtgcctgccca 200
 tccgtttctga gaaggagccg ctgcccgttc ggggagcggc aggtaggtgg 250
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 caagcccgct ccgcaggtgc gcaccttcgc cgggaaggtc tatgccttgg 500
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<210> 602

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 602

cgttcgtgca gcgtgtgta 19

<210> 603

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<223> Synthetic oligonucleotide probe

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<210> 604
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<210> 607
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<400> 609
cgactccctg agcgagcaga ttcc 25

<210> 610
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 610
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<210> 611
<211> 2840
<212> DNA
<213> Homo Sapien

<400> 611
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aacaacacc aacaactggg gtggggggaa gaaagaaaga aaagaaacc 150
accaccccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 200
ctgtggcgcg ccgcctggtt cccgggaaga ctgccagca ccagggggtg 250
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ggacatgatg ctgttggtgc aggggtgctt ttgctcgaac cagtggctgg 350
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 tgggacgttt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612
 <211> 352
 <212> PRT
 <213> Homo Sapien

<400> 612
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 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn
 35 40 45
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
 50 55 60
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
 65 70 75
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
 80 85 90
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr

110	115	120
Gln His Thr Pro Arg Thr Met Gln Val	His Leu Thr Val Gln Val	
125	130	135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn	Asp Met Thr Val Asn Glu	
140	145	150
Gly Thr Asn Val Thr Leu Thr Cys Leu	Ala Thr Gly Lys Pro Glu	
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser	Pro Ser Ala Lys Pro Phe	
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr	Gly Ile Thr Arg Asp Gln	
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu	Asn Ala Val Ser Phe Pro	
200	205	210
Asp Val Arg Lys Val Lys Val Val Val	Asn Phe Ala Pro Thr Ile	
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr	Pro Gly Arg Ser Gly Leu	
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613

<211> 1797

<212> DNA

<213> Homo Sapien

<400> 613

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ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200
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 ctggggccat catgactgca gccacgagga ggacgcaggc gtggagtgca 1650
 gcgtctgacc cggaaaccct ttcacttctc tgctcccgag gtgtcctcgg 1700
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<210> 614

<211> 520

<212> PRT

<213> Homo Sapien

<400> 614

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				20					25					30	
Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	
				35					40					45	
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	
				50					55					60	
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	
				65					70					75	
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	
				80					85					90	
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	
				95					100					105	
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	
				110					115					120	
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	
				125					130					135	
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	
				140					145					150	
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	
				155					160					165	
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	
				170					175					180	
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	

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Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln					
				200					205					210					
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln					
				215					220					225					
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys					
				230					235					240					
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro					
				245					250					255					
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met					
				260					265					270					
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro					
				275					280					285					
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln					
				290					295					300					
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val					
				305					310					315					
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro					
				320					325					330					
Gly	Arg	Ala	Gly	Leu	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Gly	Ala	Thr					
				335					340					345					
Gly	Leu	Lys	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Leu	Gln	Gly	Gln	Gln					
				350					355					360					
Gly	Arg	Lys	Gly	Glu	Ser	Gly	Val	Pro	Gly	Pro	Ala	Gly	Val	Lys					
				365					370					375					
Gly	Glu	Gln	Gly	Ser	Pro	Gly	Leu	Ala	Gly	Pro	Lys	Gly	Ala	Pro					
				380					385					390					
Gly	Gln	Ala	Gly	Gln	Lys	Gly	Asp	Gln	Gly	Val	Lys	Gly	Ser	Ser					
				395					400					405					
Gly	Glu	Gln	Gly	Val	Lys	Gly	Glu	Lys	Gly	Glu	Arg	Gly	Glu	Asn					
				410					415					420					
Ser	Val	Ser	Val	Arg	Ile	Val	Gly	Ser	Ser	Asn	Arg	Gly	Arg	Ala					
				425					430					435					
Glu	Val	Tyr	Tyr	Ser	Gly	Thr	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Glu					
				440					445					450					
Trp	Gln	Asn	Ser	Asp	Ala	Ile	Val	Phe	Cys	Arg	Met	Leu	Gly	Tyr					
				455					460					465					
Ser	Lys	Gly	Arg	Ala	Leu	Tyr	Lys	Val	Gly	Ala	Gly	Thr	Gly	Gln					

470

475

480

Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu
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Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His
500 505 510

Glu Glu Asp Ala Gly Val Glu Cys Ser Val
515 520

<210> 615

<211> 647

<212> DNA

<213> Homo Sapien

<400> 615

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atttaagaag catcctctgc caagaccaa aggaagaag aaaaagggcc 150
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gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaa 647

<210> 616

<211> 98

<212> PRT

<213> Homo Sapien

<400> 616

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Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
20 25 30

Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80					85					90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

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aggaatttat gatgctctgt ttgatattga aagcaaagtg gacccttcca 2350
aggcctgggg agaagtgaag agacagattt atgttcagc cttcacagt 2400

Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val	215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val Lys	230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg	245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro	260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu	275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr	290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro	305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val Gly	320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met His	335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly	365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr Ile	440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp	455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu	485	490	495

Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro
500		505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe
515		520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn
530		535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val
545		550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe
560		565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe
575		580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr
590		595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser
605		610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp
620		625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys
635		640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val
650		655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe
665		670	675
Ile Asp Pro Leu	Gly Leu Pro Asp Arg	Pro Phe Tyr Arg His	Val
680		685	690
Ile Tyr Ala Pro	Ser Ser His Asn Lys	Tyr Ala Gly Glu Ser	Phe
695		700	705
Pro Gly Ile Tyr	Asp Ala Leu Phe Asp	Ile Glu Ser Lys Val	Asp
710		715	720
Pro Ser Lys Ala	Trp Gly Glu Val Lys	Arg Gln Ile Tyr Val	Ala
725		730	735
Ala Phe Thr Val	Gln Ala Ala Ala Glu	Thr Leu Ser Glu Val	Ala
740		745	750

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